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OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 18:08:33 ; Search time 2979 Seconds
(without alignments)
11253.661 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggccaagccctgcctg.....aaaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
al number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_esthc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1559.6	75.3	3859	11 AK014464	AK014464 Mus muscu
2	991.6	47.9	1114	9 AF150387	AF150387 AF150387
3	958.2	46.3	2503	11 AK014390	AK014390 Mus muscu
4	819.6	39.6	913	14 BQ949536	BQ949536 AGENCOURT
5	746	36.0	747	14 BQ018588	BQ018588 UI-H-DH1-
6	740.6	35.8	1059	13 BI084083	BI084083 602869445

c	7	723.8	35.0	865	13	BI084878
	8	713.8	34.5	761	13	BM016288
	9	690.2	33.3	904	10	BE378929
	10	688.6	33.3	700	9	AL570757
	11	681.4	32.9	718	12	BF057677
	12	675.6	32.6	945	14	BQ669630
	13	657.8	31.8	684	12	BF338951
	14	644.2	31.1	730	13	BM048418
	15	633	30.6	789	12	BF204338
	16	631	30.5	840	12	BE885725
	17	624	30.1	635	10	BE296749
	18	597	28.8	684	10	AV725513
	19	595	28.7	623	13	BI828125
	20	591.6	28.6	862	13	BI157614
	21	587.6	28.4	644	12	BE783981
	22	575.8	27.8	720	12	BG288435
	23	574.2	27.7	649	12	BE837592
	24	558	27.0	939	12	BF203806
	25	525	25.4	525	9	AI005033
	26	515.2	24.9	541	10	AW770546
	27	511.4	24.7	513	14	BQ637035
	28	508	24.5	864	12	BE872035
	29	486.2	23.5	514	12	BF439471
	30	477.8	23.1	605	12	BE793449
	31	472	22.8	487	13	BM313609
	32	464	22.4	464	9	AA701598
	33	464	22.4	464	9	AI127789
	34	453.2	21.9	458	9	AL700814
	35	448	21.6	542	10	AV667139
	36	447.4	21.6	537	13	BG927600
	37	445	21.5	461	9	AL700831
	38	444	21.4	444	9	AI095556
	39	443	21.4	443	9	AI127822
	40	441.8	21.3	493	12	BF443234
	41	440.6	21.3	447	10	AW015855
	42	435.8	21.1	1092	13	BM454007
	43	426.4	20.6	428	9	AI094243
	44	425.8	20.6	573	12	BE799078
	45	421.8	20.4	425	9	AI857994

ALIGNMENTS

RESULT 1	AK014464	3859 bp	musculus	16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04	linear	HTC 19-JAN-2002
LOCUS	AK014464					
DEFINITION	AK014464					
ACCESSION	AK014464					
VERSION	AK014464.1					
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (strain:C57BL/6J) 16 days embryo head cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	Carninci,P. and Hayashizaki,Y.					
TITLE	High-efficiency full-length cDNA cloning					
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)					
MEDLINE	99279253					
PUBMED	10349636					
REFERENCE						
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.					
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)					
MEDLINE	20499374					
PUBMED	11042159					

Best Local Similarity 97.48; Pred. No. 4.6e-148; Matches 1093; Conservative 0; Mismatches 19; Indels 10; Gaps 8;			
QY	712	GGAGGTATGACCACTCGCTGTACACAGGAGTCTCTGTGTATACACCCATCCGCGGGAG	771
Db	1	GGAGGTATGACCACTCGCTGTACACAGGAGTCTCTGTGTATACACCCATCCGCGGGAG	60
QY	772	TGTTATTATGAGTTCATCTATGTCGGGTGGAGATCAATGGACAGATCTGAATGGAC	831
Db	61	TGTTATTATGAGTTCATCTATGTCGGGTGGAGATCAATGGACAGATCTGAATGGAC	120
QY	832	TGCAAGAGTACATGACAGAGATGTCGACAGTGCACACCAACCACTTCGTTTG	891
Db	121	TGCAAGAGTACATGACAGAGATGTCGACAGTGCACACCAACCACTTCGTTTG	180
QY	892	CCCAAGAAAGTGTGTTGAAGTGCAGTCAATCCATCAAGGAGGCTCTCCACGGAGAAG	951
Db	181	CCCAAGAAAGTGTGTTGAAGTGCAGTCAATCCATCAAGGAGGCTCTCCACGGAGAAG	240
QY	952	TTCCCTGATGTTTCTGGCTAGGAGACAGTGTGTGCTGGCAAGGAGCACCACCCCT	1011
Db	241	TTCCCTGATGTTTCTGGCTAGGAGACAGTGTGTGCTGGCAAGGAGCACCACCCCT	300
QY	1012	TGGAACATTTTCCAGTCATCTACTTACCTAATGGGTGAGGTTACCAACCACTCTTC	1071
Db	301	TGGAACATTTTCCAGTCATCTACTTACCTAATGGGTGAGGTTACCAACCACTCTTC	360
QY	1072	CGATACCATCTTCCGACGACATPACCTGGCGGCGAGTGGAGATGTGGCCAGTCCCAA	1131
Db	361	CGATACCATCTTCCGACGACATPACCTGGCGGCGAGTGGAGATGTGGCCAGTCCCAA	419
QY	1132	GACGACTGTCAAGTGTGTCATCTCACAGTCATCCAGCGGCACTGTATGGGAGCTGT	1191
Db	420	GACGACTGTAC-AGTGTGTCATCTCACAGTCATCCAGCGGCACTGTATGGGAGCTGT	478
QY	1192	ATCATGAGGGGCTTCTA-CGTTGTCTTTGATCGGGCCGGAAGAAATGTGCTTGTGT	1250
Db	479	ATCATGAGGGGCTTCTACCGTGTCTTTGATCGGGCCGGAAGAAATGTGCTTGTGT	538
QY	1251	CAGCGCTTGCCATGTGCAGATGAGTTCAGGAGCGCAGCGTGGAAAGCCCTTTTGTGAC	1310
Db	539	CAGCGCTTGCCATGTGCAGATGAGTTCAGGAGCGCAGCGTGGAAAGCCCTTTTGTGAC	597
QY	1311	CTTGACATGGAAGACTGTGGTACACATTCACAGACAGATGATCAACCTCATGAC	1370
Db	598	CTTGACATGGAAGACTGTGGTACACATTCACAGACAGATGATCAACCTCATGAC	657
QY	1371	CATAGCTATGATGGCTGCCATCTCGCCCTCTTCATGTCGACCTCGCCTCATGCT	1430
Db	658	CATAGCTATGATGGCTGCCATCTCGG-CCTCTTCATGCTGCGCCTCTGCTCATGCT	716
QY	1431	GTGTGAG-TGGCGCTGCCCTGCCCTGCCGAGCAGCATGATGACTTTGCTGATGACA	1489
Db	717	GTGTGAG-TGGCGCTGCCCTGCCCTGCCGAGCAGCATGATGACTTTGCTGATGACA	776
QY	1490	FTCCCTGCTGAAGTGAAGAGGCCATGGGAGAGATAGAGATTCCTCCCTGGACACACC	1549
Db	777	FTCCCTGCTGAAGTGAAGAGGCCATGGGAGAGATAGAGATTCCTCCCTGGACACACC	836
QY	1550	TCGCTGTTTCACTTTGTTGCACAGTAGGAGACACAGATGGCAGCTGTGGCCAGACCT	1609
Db	837	TAGTGTGCTACCTTTGGCAGC-AGTAGGAGACACAGATGGCAGCTGTGGCCAGACCT	893
QY	1610	CAGGACCTTCCACCCACCAATGCTCTGCTTGTGAGAGAGAGAAAGCTGGCAG	1669
Db	894	CAGGACCTTCCACCCACCAATGCTCTGCTTGTGAGAGAGAGAAAGCTGGCAG	953
QY	1670	GTGGTTCAGGAGTGTACCTGTAGGAACAGAAAGAGAAAGAGGACTCTGCTG	1729
Db	954	GTGGTTCAGGAGTGTACCTGTAGGAACAGAAAGAGAAAGAGGACTCTGCTG	1012
QY	1730	GCAGGAATACTCTTGTGCTACCTCAAAATTTAAGTCGGGAAATTTCTGCTGTTGAAACTTCA	1789

Db	1013	CGGGGAATACTCTTGGTCACCTCAAAATTAAGTCGGAATAATCTGCTCTGAAACTTCA	1072
Qy	1790	GCCTGGAACCTTTGTCACCATTCCTTTAAATCTTCAACCC	1831
Db	1073	ACCTGGAACCTTTGTCACCATTCCTTTAAATATATACACCC	1114
RESULT 3			
LOCUS	AK014390	2503 bp	mRNA linear HTC 19-JAN-2002
DEFINITION	Mus musculus adult male brain cDNA, RIKEN full-length enriched library, clone:3526402A15:beta-site APP cleaving enzyme, full insert sequence.		
ACCESSION	AK014390		
VERSION	AK014390.1	GI:12852207	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male brain cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library clone:3526402A15.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	1		
TITLE	Carninci, P. and Hayashizaki, Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, C., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		
PUBMED	11217851		

1722	CTCTGCTGGCGGGAATACTCTTGGTCACCTCAAAATTAAGTCGGGAAATTCGTCTGCTTGG	1781
Db		1782
1723	TTCTGGTGGCAGGAATATCCTTAGACACCAACAACCTTGAGT-TGGAAATTTTGCTGCTTG	1782
Db		1783
1724	AAACTTCAGCCCTGAAACCTTTGTGCCACCAATTCCTTTAAATTTCTCCAAACCAAGTATTCT	1841
QY		1842
1725	AAGCTTCAGCCCTGACCCCTCTGCCAGCA-TCCTTTAGAGTCTCCAACCTTAAAGTATTCT	1842
Db		1843
1726	TCTTTTCTTTAGTTTCAGAAGTACTGCAATCACACGCAGGTACTCTTGGCGTGTGCCCTG	1901
QY		1902
1727	TTATGTC---CTCCAGAAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTG	1901
Db		1903
1728	TGTTACCCCTGGCAGAGAAAGACCAAGCTGTGTTTCCTGCTGGCCAAAGTCAGTAGGAGA	1961
QY		1962
1729	TGTTACCCCTGGCAGAGAAAGGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAGA	1961
Db		1963
1730	GGATGCACATGTGCTTATTTGCTTTTAGACACGGGACTGPTATAACAAGGCTTAACATTGG	2021
QY		2022
1731	--AAGTGAAGTTTGGCAGATTGCTTTAGTAGAGGACTGCAGACTCAAGCCT-ACACTGG	2021
Db		2023
1732	TCGAAAGATTGCCTCTTGAATTTAAAAAAA	2052
QY		2053
1733	TACAAAGACTGCGCTCTTGAGATAAACAGAA	1340
Db		1341

RESULT	4
BQ949536	
LOCUS	913 bp mRNA linear EST 21-AUG-2002
DEFINITION	ACGNCOURT_8733256 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6454803 5', mRNA sequence.
ACCESSION	BQ949536
VERSION	BQ949536.1 GI:22365014
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS	Unpublished (1999)
TITLE	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov
JOURNAL	Tissue Procurement: ATCC
COMMENT	cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2632 row: h column: 04 High quality sequence stop: 613.

BASE COUNT	207 a	259 c	232 g	206 t	9 others
ORIGIN					
Query Match			39.6%	Score 819.6;	DB 14; Length 913;

[illegible]

RESULT 5	BQ018588	747 bp	linear	EST 27-MAR-2000
LOCUS	BQ018588/c			
DEFINITION	UI-H-187-awu-c-12-0-UI.sl NCL_CGAP_DHL Homo sapiens CDNA clone			
ACCESSION	BQ018588			
VERSION	BQ018588.1			
KEYWORDS	EST.			
SOURCE	human.			

(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT	243 a	300 c	273 g	243 t
ORIGIN				
Query Match	35.8%;	Score 740.6;	DB 13;	Length 1059;
Best Local Similarity	92.5%;	Pred. No. 3e-108;		
Matches	837;	Conservative 0;	Mismatches 54;	Indels 14; Gaps 5;
QY	852	CAAGAGCATTTGGACAGTGGCCACCAACCTTCGTTGGCCCAAGAAAGTTTGAAGC	911	
Db	2	CAAGAGCATTTGGACAGTGGCCACCAACCTTCGTTGGCCCAAGAAAGTTTGAAGC	61	
QY	912	TGCAGTCAATTCATCAAGGAGGCTCTCCACGAGAGTTCCTGATGGTTCTGGCT	971	
Db	62	TGCAGTCAATTCATCAAGGAGGCTCTCCACGAGAGTTCCTGATGGTTCTGGCT	121	
QY	972	AGGAGAGCAGTGGTGTCTGGCAAGCAGCACCACCTTGGAAACATTTTCCAGTCAT	1031	
Db	122	AGGAGAGCAGTGGTGTCTGGCAAGCAGCACCACCTTGGAAACATTTTCCAGTCAT	181	
QY	1032	CTCACTCTACCTAATGAGGTGAGTTACCAACAGTCTCTTCGCGATCACCATCTTCGCA	1091	
Db	182	CTCACTCTACCTAATGAGGTGAGTTACCAACAGTCTCTTCGCGATCACCATCTTCGCA	241	
QY	1092	GCAATACCTGGCCAGTGGAGATGTGCCACGTCCTCCCAAGCAGCTGTACAAGTTTG	1151	
Db	242	GCAATACCTGGCCAGTGGAGATGTGCCACGTCCTCCCAAGCAGCTGTACAAGTTTG	301	
QY	1152	CATCTCACAGTCATCCAGGGGACCTGTTATGGAGCTGTTATCATGAGGCGCTTCTAGT	1211	
Db	302	CATCTCACAGTCATCCAGGGGACCTGTTATGGAGCTGTTATCATGAGGCGCTTCTAGT	361	
QY	1212	TGCTTTTATCGGGCCGAAACGAATTTGGCTTGTCTGACGCGCTTCCATGTCACGA	1271	
Db	362	TGCTTTTATCGGGCCGAAACGAATTTGGCTTGTCTGACGCGCTTCCATGTCACGA	421	
QY	1272	TGAGTTCAGGCGGAGCGGTGGAAGCGCTTTTGTCACTTGGACATGGAAGCTGTGG	1331	
Db	422	TGAGTTCAGGCGGAGCGGTGGAAGCGCTTTTGTCACTTGGACATGGAAGCTGTGG	481	
QY	1332	CTACAACATTCACAGACAGATGATCAACCTCATGACCATAGGCTATGTCATGGCTGC	1391	
Db	482	CTACAACATTCACAGACAGATGATCAACCTCATGACCATAGGCTATGTCATGGCTGC	541	
QY	1392	CATCTCGCCCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1451	
Db	542	CATCTCGCCCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	601	
QY	1452	CTGCTTGGCCAGCAGCATGATGCTTGTGCTGATGACATCTCCCTGCTGAAGTGAAGG	1511	
Db	602	CTGCTTGGCCAGCAGCATGATGCTTGTGCTGATGACATCTCCCTGCTGAAGTGAAGG	661	
QY	1512	CCATGGGAGAGATAGAGATTCCTGCTGGACACACCTCCGCTGCTGCTGCTGCTGCT	1571	
Db	662	CCATGGGAGAGATAGAGATTCCTGCTGGACACACCTCCGCTGCTGCTGCTGCTGCT	721	
QY	1572	AGTAGGAGACAGATGGACCTGTGGCCAGAGCAGCTCAGGACCTCCCCACCCACCA	1631	
Db	722	AGTAGGAGACAGATGGACCTGTGGCCAGAGCAGCTCAGGACCTCCCCACCCACCA	778	
QY	1632	ATGCCCTCTGCTTGTAGAGAGAAAGCTGGCAAGTGGTGGTTCAGGGGACTGTACCT	1691	
Db	779	ATGCCCTCTGCTTGTAGAGAGAAAGCTGGCAAGTGGTGGTTCAGGGGACTGTACCT	833	
QY	1692	GTAGGAACAGAAAGAGAGAAAGAGACCTCTGCTGGCGGGAATACCTCTTGGTCACT	1751	
Db	834	GTAGGAACAGAAAGAGAGAAAGAGACCTCTGCTGGCGGGAATACCTCTTGGTCACT	887	
QY	1752	CAAAAT 1756		
Db	888	AAATT 892		

RESULT 7
BI084878/c
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

BI084878 865 bp mRNA linear EST 20-JUN-2001
602869445T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013994 3',
mRNA sequence.
BI084878
BI084878.1 GI:14503208
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI820 row: j column: 11
High quality sequence start: 18
High quality sequence stop: 821.

Location/Qualifiers
1. 865
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5013994"
/clone_lib="NIH_MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 207 a 224 c 228 g 205 t 1 others

Query Match 35.0%; Score 723.8; DB 13; Length 865;
Best Local Similarity 95.3%; Pred. No. 1.5e-105;
Matches 810; Conservative 0; Mismatches 33; Indels 7; Gaps 6;

QY	1108	GTGGAAGATGTGGCCACGTCCTCCCAAGACGACTGTTACAGTTGGCCATCTCACAGTCATCC	1167	
Db	865	GTGGAAGATGTGGCCACGTCCTCCCAAGACGACTGTTAC-AGGTTGCCATCTCACAGTCATCC	807	
QY	1168	ACGGGCACTGTATGGGAG-CTGTTATCATGAGGCTTCTACCTTGTCTTTGATCGGC	1226	
Db	806	ACGGCACTGTATGGGAGCTGTTATCATGGAGGCTTCTACCTTGTCTTTGATCGGC	747	
QY	1227	CCGAAAACGAATTTGGCTTGTGTGTCAGGCTTGCCA-TGTGCACGATGAGTTCAGGACGG	1285	
Db	746	CCGAAAACGAATTTGGCTTGTGTGTCAGGCTTGCCATTTGTCACGATGAGTTCAGGACGG	687	
QY	1286	CAGCGGTGGAAGGCGCTTTTGTACCTTGGACATGGAGACTGTGGC--TACACATTC	1343	
Db	686	CAGCGGTGGAAGGCGCTTTTGTCTCTGGACATGGAGACTGTGGCATAACATTC	627	
QY	1344	ACAGACAGATGATGATCAACCCCTCATGACCATAGCCCTATGTCATGGCTGCGCCT	1403	
Db	626	ACAGACAGATGATGATCAACCCCTCATGACCATAGCCCTATGTCATGGCTGCGCCT	567	

Thu Jul 10 16:10:59 2003

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ACCESSION BE378929
VERSION BE378929.1 GI:9324294
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csaasb@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM264 row: g column: 08
High quality sequence stop: 735.
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/lab_host="DH10B (phage-resistant)"
/Note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
191 a 240 c 256 g 217 t

BASE COUNT
ORIGIN
Query Match 33.3%; Score 690.2; DB 10; Length 904;
Best Local Similarity 98.1%; Pred. No. 3.2e-100;
Matches 741; Conservative 0; Mismatches 8; Indels 6; Gaps 4;

QY 749 GGTATACACCCATCCGGGGAGTGGTATTATAGGT-CATCATGTCCGGGTGGAGATC 807
DB 1 GGTATACACCCATCCGGGGAGTGGTATTATAGGTCCATCATGTCCGGGTGGAGATC 60
808 AATGACAGGATCTGAAATGACTGCAAGGAGTACAACTATGACAGGATTTGGAC 867
DB 61 AATGACAGGATCTGAAATGACTGCAAGGAGTACAACTATGACAGGATTTGGAC 120
868 AGTGCACCAACCACTCTGTTTCCCAAGAGTGTGAAGCTGCAGTCAAAATCCATC 927
DB 121 AGTGCACCAACCACTCTGTTTCCCAAGAGTGTGAAGCTGCAGTCAAAATCCATC 180
QY 928 AA-GGCAGCCTCTCCACGAGAGTTCCTGATGTTTCTGGCTAGGAGACAGCTGGT 986
DB 181 AAGGCAGCCTCTCCACGAGAGTTCCTGATGTTTCTGGCTAGGAGACAGCTGGT 240
QY 987 GTGCTGGCAAGCAGGACCAACCCCTTGGACATTTCCAGTCATCTCACTACCTAAT 1046
DB 241 GTGCTGGCAAGCAGGACCAACCCCTTGGACATTTCCAGTCATCTCACTACCTAAT 300
1047 GGTGAGGTATACCAACCACTCTCCGATACCACTCTCCGAGCAATACCTCGGCC 1106
DB 301 GGTGAGGTATACCAACCACTCTCCGATACCACTCTCCGAGCAATACCTCGGCC 360
QY 1107 AGTGAAGATGTGGCCACGTCCTCCCAAGACGACTGTGTACAGTTTGGCATCTCACATCATC 1166
DB 361 AGTGAAGATGTGGCCACGTCCTCCCAAGACGACTGTGTACAGTTTGGCATCTCACATCATC 420
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DB 421 CACGGGCAGTGTATGGGAGCTTTATCATGAGGGCTTCTACGTTGTCTTTGATCGGC 480
QY 1227 CCGAAACGAATGGCTTTGCTGTCAGCGCTTGCATGTGCAGATGAGTTTCAGGACGC 1286
DB 481 CCGAAACGAATGGCTTTGCTGTCAGCGCTTGCATGTGCAGATGAGTTTCAGGACGC 540
QY 1287 AGCGGTGGAAGCCCTTTTGTCCACCTTGGACATGGAAGACTGTGGCTACAAATTCACCA 1346
DB 541 AGCGGTGGAAGCCCTTTTGTCCACCTTGGACATGGAAGACTGTGGCTACAAATTCACCA 600
QY 1347 GACAGATGAGTCAACCCCTCATGACATAGCCTATGTATGCTGCTGCATCGCCCTCTT 1406
DB 601 GACAGATGAGTCAACCCCTCATGACATAGCCTATGTATGCTGCTGCATCGCCCTCTT 660
QY 1407 CATGCTGCCACTTGCCTCATGCTGTGTGTCAGTGGGCTGCCCTGCCCTGCTGCGCAGCA 1466
DB 661 CATGCTG-CACVCTGCCCTCATGCTGTGTCAGTGGGCTG---CTCCGCTGCTGCGCAGCA 716
QY 1467 GCATGATGACTTTGGTGTGATGACATTCCTCTGTGA 1501
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RESULT 10
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DEFINITION prime, mRNA sequence.
ACCESSION AL570757
VERSION AL570757.1 GI:12927378
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 169 a 173 c 191 g 161 t 6 others
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Query Match 33.3%; Score 688.6; DB 9; Length 700;
Best Local Similarity 99.3%; Pred. No. 6.5e-100;
Matches 688; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1310 CTTTGGACATGGAAGACTGTGGCTTACAACTTCCACAGACAGATGATTCACCCCTCATGA 1369

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RESULT 12	BO669630	NIH-MGC	945 bp	mRNA	linear	EST 15-JUL-2002
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DEFINITION	5', mRNA sequence.					
ACCESSION	BO669630					
VERSION	BO669630.1	GI:21780464				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 945)					
TITLE	NIH-MGC http://mgc.nci.nih.gov/					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999)					
	Contact: Robert Strausberg, Ph.D.					
	Email: egapbs@email.nih.gov					
	Tissue Procurement: ATCC					
	cDNA Library Preparation: Rubin Laboratory					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Agencourt Bioscience Corporation					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNL at:					
	http://image.llnl.gov					
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	/lab_host="DH10B (phage-resistant)"					
	/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;					
	cDNA made by oligo-dT priming.					
	Site_2: EcoRI; cDNA made by oligo-dT priming.					
	Directionally cloned into EcoRI/XhoI sites using the					
	following 5' adaptor: GGACGAG(G). Library constructed					
	by Ling Hong in the laboratory of Gerald M. Rubin					
	(University of California, Berkeley) using ZAP-cDNA					
	synthesis kit (Stratagene) and Superscript II RT (Life					
	Technologies). Note: this is a NIH_MGC Library."					
BASE COUNT	253 a	231 c	245 g	214 t	2 others	
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Best Local Similarity	99.0%; Pred. No. 6.5e-98;					
Matches	689; Conservative	0; Mismatches	6; Indels	1; Gaps	1; Gaps	1;
Qy	1365	CATGACCATAGCCATGTCATGGCTGCATCGCCCTCTTCATGTCGCCACTTCGCT	1424			
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Qy	1425	CATGCTGTGTCAGTGGCGCTCCGCTCGCTCGCCAGCAGCATGATGACTTTGGTGA	1484			
Dd	61	CATGCTGTGTCAGTGGCGCTCCGCTCGCTCGCCAGCAGCATGATGACTTTGGTGA	120			
Qy	1485	TGACATCTCCCTGCTGAAGTGAGGAGGCCATGGCGAAGATAGAGATTCCTCGGACC	1544			
Dd	121	TGACATCTCCCTGCTGAAGTGAGGAGGCCATGGCGAAGATAGAGATTCCTCGGACC	180			
Qy	1545	ACACCTCGGTGTTTCACATTTGGTTCACAAAGTAGGAGACACAGATGSCACCTTGCCAGAG	1604			
Dd	181	ACACCTCGGTGTTTCACATTTGGTTCACAAAGTAGGAGACACAGATGSCACCTTGCCAGAG	240			
Qy	1605	CACCTCAGAGCCTCCCAACCCACCAATGCTTCGCTTCATGGAGAAGGAAAGGCTG	1666			
Dd	241	CACCTCAGAGCCTCCCAACCCACCAATGCTTCGCTTCAT				

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QY 1289 CGGTGGAAGGCCCTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATCCACAGA 1348
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QY 1409 TGCTGCACACTGCTCCTATGTGTGTCAGTGGCGCTCCTCGCTGCTGCTGGCCAGCAGC 1468
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Db 361 GCACCTGTGGCAGAGCAGCCTCAGGACCTCCGCCACCCACCAATGCTCTGCTGATG 420
QY 1649 GAGAAGGAAGAGCTGCTGCTGGCGGGAATCTCTTGTGCTCACTTGTAGGAGACACAAAGA 1708
Db 421 GAGAAGGAAGAGCTGCTGCTGGCGGGAATCTCTTGTGCTCACTTGTAGGAGACACAAAGA 479
QY 1709 GAAGAAAGAAAGCCTCTGCTGGCGGGAATCTCTTGTGCTCACTTGTAGGAGACACAAAGA 1768
Db 480 GAAGAAAGAAAGCCTCTGCTGGCGGGAATCTCTTGTGCTCACTTGTAGGAGACACAAAGA 539
QY 1769 ATCTGCTGTGAACTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAAC 1828
Db 540 ATCTGCTGTGAACTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAAC 599
QY 1829 CCC-AAAGTATCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1887
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DEFINITION 603625683f1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452052 5',
mRNA sequence.
ACCESSION BM048418
VERSION BM048418.1 GI:16777685
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcgaps@remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1CM1943 row: f column: 21
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/note="Organ: prostate; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 163 a 210 c 206 g 151 t
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Best Local Similarity 96.7%; Pred. No. 7e-93;
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QY 234 GATGACCGTGGCAGCCCGCAGAGCGCTCAACATCTGCTGTGATACAGGACGAGTAA 293
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QY 294 CTTTGCAGTGGGTGCTGCCCGCCACCCCTTCCTGCATGGCTTACCAGAGGAGCTGTC 353
Db 61 CTTTGCAGTGGGTGCTGCCCGCCACCCCTTCCTGCATGGCTTACCAGAGGAGCTGTC 120
QY 354 CAGCACATACCGGACCTCCCGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGA 413
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QY 414 AGGGAGCTGGGACCCAGCCTGGTAAGCATCCCCCATGGCCCCCAACGCTCACTGTGCGTGC 473
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QY 474 CAACATTTGCTGCCATCACTGAATCAGACAAAGTTTTCATCAACGGCTCCAACTGGGAAG 533
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QY 534 CATCTGGGCTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGGCTTCTT 593
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QY 774 GTATTATGAGTCTATCTTGTGCGGGTGGAGATCAATGGAGGAGGATCTGAAATGGAGCTG 833
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mRNA sequence.
ACCESSION BF204338
VERSION BF204338.1 GI:11097924
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 789)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM987 row: e column: 03
High quality sequence stop: 716.
Location/Qualifiers
1..789
/organism="Homo sapiens"
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/note="Organ: muscle; Vector: pOTB7; Site:1: EcoRI;
Site:2: XhoI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
180 a 204 c 215 g 190 t

FEATURES
source

241 ATTTTCCCGAGTCATCTCACTACCTAATGGGTGAGGTACCAACCAAGCTCTCTCCGCATC 300
QY 1078 ACCATCCTTCCGCAGCAATACCTGGCCAGTGGGAAGATGTGGCACGCTCCCAAGACGAC 1137
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QY 1138 TGTTACAAAGTTTGCCATCTCACAGTCATCCAGGSCACTGTTATGGGAGCTGTTATCATG 1197
Db 361 TGTTACAAAGTTTGCCATCTCACAGTCATCCAGGSCACTGTTATGGGAGCTGTTATCATG 420
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Search completed: July 8, 2003, 19:45:54
Job time : 2985 secs

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Best Local Similarity 99.6%; Pred. No. 4e-91;
Matches 666; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

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3	2032	98.2	2541	4	US-09-009-191-1	Sequence 1, Appli
4	1887.2	91.2	1977	4	US-09-548-372D-5	Sequence 5, Appli
5	1887.2	91.2	1977	4	US-09-548-367D-5	Sequence 5, Appli
6	1843.4	89.1	2370	4	US-09-009-191-3	Sequence 3, Appli
7	1752.4	75.0	2043	4	US-09-548-372D-7	Sequence 7, Appli
8	1552.4	75.0	2043	4	US-09-548-367D-7	Sequence 7, Appli
9	1359	65.7	1362	4	US-09-548-372D-29	Sequence 29, Appl
10	1359	65.7	1362	4	US-09-548-367D-29	Sequence 29, Appl
11	1359	65.7	1380	4	US-09-548-372D-31	Sequence 31, Appl
12	1359	65.7	1380	4	US-09-548-367D-31	Sequence 31, Appl
13	1297	62.7	1341	4	US-09-548-372D-21	Sequence 21, Appl
14	1297	62.7	1341	4	US-09-548-367D-21	Sequence 21, Appl
15	1297	62.7	1380	4	US-09-548-372D-23	Sequence 23, Appl
16	1297	62.7	1380	4	US-09-548-367D-23	Sequence 23, Appl
17	1294.8	62.6	1506	4	US-09-713-158-1	Sequence 1, Appli
18	1273.6	61.5	1302	4	US-09-548-372D-25	Sequence 25, Appl
19	1273.6	61.5	1302	4	US-09-548-367D-25	Sequence 25, Appl
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21	1199	57.9	1287	4	US-09-548-367D-50	Sequence 50, Appl
22	1199	57.9	1305	4	US-09-548-372D-52	Sequence 52, Appl
23	1199	57.9	1305	4	US-09-548-367D-52	Sequence 52, Appl
24	1183.2	57.2	1278	4	US-09-548-372D-27	Sequence 27, Appl
25	1183.2	57.2	1278	4	US-09-548-367D-27	Sequence 27, Appl
26	421.2	20.3	511	4	US-09-280-116-30	Sequence 30, Appl
27	393.4	19.0	1545	4	US-09-717-432-1	Sequence 1, Appli

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QY	361	TACCGGACCTCCGAAGGGTGTGTATGTGCCCTACCCAGGGCAAGTGGAAAGGGGAG	420
Db	361	TACCGGAGCCTCCGAAGGGTGTGTATGTGCCCTACCCAGGGCAAGTGGAAAGGGGAG	420
QY	421	CTGGGCACCGACCTGTTAAGCATCCCCAAGCTCCCTGACGTCTGTCGGTGGCCAACTT	480
Db	421	CTGGGCACCGACCTGTTAAGCATCCCCAAGCTCCCTGACGTCTGTCGGTGGCCAACTT	480
QY	481	GCTGCCATCACTGAATCAGACAAGTCTTCATCAACGGCTCCAACTGGGAAGGATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTCTTCATCAACGGCTCCAACTGGGAAGGATCCTG	540
QY	541	GGCTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT	600
Db	541	GGCTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT	600
QY	601	CTGGTAAAGCAGACCGTTCCTCAACCTTCTCTCCCTGCACCTTTGTGGTCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCGTTCCTCAACCTTCTCTCCCTGCACCTTTGTGGTCTGGCTTC	660
QY	661	CCCTCAACAGTCTGAAGTGTCTGGCTCTGTCGGAGGAGCATGATCATTTGAGGATATC	720
Db	661	CCCTCAACAGTCTGAAGTGTCTGGCTCTGTCGGAGGAGCATGATCATTTGAGGATATC	720
QY	721	GACCACTCGCTGTACACAGCAGTCTGTGTATACACCATCCGGGGGAGTGTATTAT	780
Db	721	GACCACTCGCTGTACACAGCAGTCTGTGTATACACCATCCGGGGGAGTGTATTAT	780
QY	781	GAGTCTCATCTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGAG	840
Db	781	GAGTCTCATCTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGAG	840
QY	841	TACAACATATGACAAGAGCATTTGGACAGTGGCACCAACCAACCTTCGTTTGCCCAAGAA	900
Db	841	TACAACATATGACAAGAGCATTTGGACAGTGGCACCAACCAACCTTCGTTTGCCCAAGAA	900
QY	901	GTGTTTGAAGTGCAGTCAATCCATCAAGCAGCCTCTCCACGAGAGAGTTTCCCTGAT	960
Db	901	GTGTTTGAAGTGCAGTCAATCCATCAAGCAGCCTCTCCACGAGAGAGTTTCCCTGAT	960
QY	961	GGTTTCTCGCTTAGGAGAGCAGTGGTGTGTGCAAGCAGGACCAACCCCTTGGACATTT	1020
Db	961	GGTTTCTCGCTTAGGAGAGCAGTGGTGTGTGCAAGCAGGACCAACCCCTTGGACATTT	1020
QY	1021	TTCCGAGTCTCACTCTACCTAATGGGTGAGGTTACCAACCAAGTCCCTTCGCGATCAC	1080
Db	1021	TTCCGAGTCTCACTCTACCTAATGGGTGAGGTTACCAACCAAGTCCCTTCGCGATCAC	1080
QY	1081	ATCCTTCGGACGAATACCTCGCGCCAGTGGAGATGTGGCCACAGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCGGACGAATACCTCGCGCCAGTGGAGATGTGGCCACAGTCCCAAGACGACTGT	1140
QY	1141	TACAAGTTTGGCATCTCACAGTCTATCCACGGGCACCTGTTATGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGGCATCTCACAGTCTATCCACGGGCACCTGTTATGGAGCTGTTATCATGGAG	1200
QY	1201	GGCTTCTACGTGTCTTTGATCGGGCCGGAACGAATGGCTTGTGCTGCAGCGTTGC	1260
Db	1201	GGCTTCTACGTGTCTTTGATCGGGCCGGAACGAATGGCTTGTGCTGCAGCGTTGC	1260
QY	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGCCCTTTTGTCACTTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGCCCTTTTGTCACTTTGGACATG	1320
QY	1321	GAAGACTGTGGCTACACAATTCACACAGACATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACACAATTCACACAGACATGAGTCAACCCCTCATGACCATAGCCTAT	1380

RESULT 2

US-09-548-367D-3
: Sequence 3, Application US/09548367D

Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE THEREOF

QY	1381	GT	CATGGCTGCCATCTGCGCCCTCTTTCATGCTGCCACTCTGCCTCATGTGTGTCTAGTGG	1440
DB	1381	GT	CATGGCTGCCATCTGCGCCCTCTTTCATGCTGCCACTCTGCCTCATGTGTGTCTAGTGG	1440
QY	1441	CG	TGCTCGCTGCTGCTGGCCAGCAGCATGATGACTTTGCTGATCAGACATCTCCCTGCTG	1500
DB	1441	CG	TGCTCGCTGCTGCTGGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
QY	1501	AAG	TGAGGAGGCCATCTGGCCAGAAATAGAGATTCCCTGGACACACCTCCCTGGTTCA	1560
DB	1501	AAG	TGAGGAGGCCCATGGCCAGAAATAGAGATTCCCTGGACACACCTCCCTGGTTCA	1560
QY	1561	CT	TTTGGTCACAAGTAGGAGACACAGATGGCACCCTGGCCAGACGACCTCAGGACCCCTCC	1620
DB	1561	CT	TTTGGTCACAAGTAGGAGACACAGATGGCACCCTGGCCAGACGACCTCAGGACCCCTCC	1620
QY	1621	CC	ACCACCAAAATGCCTCTGCCTTGATGGAGAGAAAGGCTGGCAAGTGGGTTCACG	1680
DB	1621	CC	ACCACCAAAATGCCTCTGCCTTGATGGAGAGAAAGGCTGGCAAGTGGGTTCACG	1680
QY	1681	GG	ACTGTACTGTAGGAACAGAAAAGAGAAAGAACGACACTCTGCTGCGGGGAATACT	1740
DB	1681	GG	ACTGTACTGTAGGAACAGAAAAGAGAAAGAACGACACTCTGCTGCGGGGAATACT	1740
QY	1741	CT	TGGTCACCTCAAAATTTAAGTCGGGAAATTCGCTCTTGTAACACTTCAGCCCTGAACCT	1800
DB	1741	CT	TGGTCACCTCAAAATTTAAGTCGGGAAATTCGCTCTTGTAACACTTCAGCCCTGAACCT	1800
QY	1801	TT	GTCACCATTCTTTAAATTCCTCAACCCCAAGTATCTCTTTTCTTAGTTTCAGAA	1860
DB	1801	TT	GTCACCATTCTTTAAATTCCTCAACCCCAAGTATCTCTTTTCTTAGTTTCAGAA	1860
QY	1861	GT	ACTGGCATCACACGAGTTACTTTGGGTGTGTCCTGTGTACCTCTGGCAGAGAAG	1920
DB	1861	GT	ACTGGCATCACACGAGTTACTTTGGGTGTGTCCTGTGTACCTCTGGCAGAGAAG	1920
QY	1921	AG	ACCAAGCTTGTTTCCTGCTGCCAAAGTCATAGGAGGATGCACAGTTTGCTATT	1980
DB	1921	AG	ACCAAGCTTGTTTCCTGCTGCCAAAGTCATAGGAGGATGCACAGTTTGCTATT	1980
QY	1981	TG	CTTTTAGACACGGGACTGTATAACCAAGCTTAACATTGGTGCAAGATTGCCTCTTTGA	2040
DB	1981	TG	CTTTTAGACACGGGACTGTATAACCAAGCTTAACATTGGTGCAAGATTGCCTCTTTGA	2040
QY	2041	AT	TAATAAAAAAAAAAAAAAAAAAAAAA	2070
DB	2041	AT	TAATAAAAAAAAAAAAAAAAAAAAAA	2070

; ORGANISM: Homo sapiens									
US-09-548-367D-3									
Query Match 99.9%; Score 2068.4; DB 4; Length 2070;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	1	ATGGCCCAAGCCCTGGCCCTGGCTCTGCTGTGATGGCGCGGAGTGCCTGCCAC	60						
Db	1	ATGGCCCAAGCCCTGGCCCTGGCTCTGCTGTGATGGCGCGGAGTGCCTGCCAC	60						
Qy	61	GGCACCAGCAGCGCATCCGGCTGCCCTGGCAGAGCGGCTGGGGGCGCCCTGGG	120						
Db	61	GGCACCAGCAGCGCATCCGGCTGCCCTGGCAGAGCGGCTGGGGGCGCCCTGGG	120						
Qy	121	CTGGGCTGCCCGGAGACCGACGAAGAGCCGAGAGCCCGCGCGAGGGGAGCTTT	180						
Db	121	CTGGGCTGCCCGGAGACCGACGAAGAGCCCGAGAGCCCGCGCGAGGGGAGCTTT	180						
Qy	181	GTGGAGATGTGGACAACTTGAGGGCAAGTGGGGCAGGGCTACTACGTGGAGATGAC	240						
Db	181	GTGGAGATGTGGACAACTTGAGGGCAAGTGGGGCAGGGCTACTACGTGGAGATGAC	240						
Qy	241	GTGGGAGCCCCCGCAGACGCTCAACATCTGTGTGATACAGCAGCAGTAACCTTGCA	300						
Db	241	GTGGGAGCCCCCGCAGACGCTCAACATCTGTGTGATACAGCAGCAGTAACCTTGCA	300						
Qy	301	GTGGGTGCTGCCCGCCACCCCTTCTGCTGCTACTACAGAGGCAAGTGGAGGGAG	360						
Db	301	GTGGGTGCTGCCCGCCACCCCTTCTGCTGCTACTACAGAGGCAAGTGGAGGGAG	360						
Qy	361	TACGGGACCTCGGAAGGTGTATGTATGCTTACACCCAGGCAAGTGGAGGGGAG	420						
Db	361	TACGGGACCTCGGAAGGTGTATGTATGCTTACACCCAGGCAAGTGGAGGGGAG	420						
Qy	421	CTGGGACCGACCTGTGAAGCATCCCAATGGCCCAAGCTGCTGCTGCGCAACATT	480						
Db	421	CTGGGACCGACCTGTGAAGCATCCCAATGGCCCAAGCTGCTGCTGCGCAACATT	480						
Qy	481	GCTGCCATCACTGAATCAGACAAGTCTTATCAACCGGCTCCAACTGGGAAGGCATCTG	540						
Db	481	GCTGCCATCACTGAATCAGACAAGTCTTATCAACCGGCTCCAACTGGGAAGGCATCTG	540						
Qy	541	GGGCTGCCCTATGCTGAGATGGCAGGCTGACGACTCCCTGGAGCCTTCTTTGACTCT	600						
Db	541	GGGCTGCCCTATGCTGAGATGGCAGGCTGACGACTCCCTGGAGCCTTCTTTGACTCT	600						
Qy	601	CTGCTAAGCAGACCCAGCTTCCCAACCTCTTCCCTGCACCTTTTGTGTGGCTTC	660						
Db	601	CTGCTAAGCAGACCCAGCTTCCCAACCTCTTCCCTGCACCTTTTGTGTGGCTTC	660						
Qy	661	CCCTCAACAGTCTGAAGTGGCTGCTGCTCGAGGGAGCATGATCGATTGGAGGTATC	720						
Db	661	CCCTCAACAGTCTGAAGTGGCTGCTGCTCGAGGGAGCATGATCGATTGGAGGTATC	720						
Qy	721	GACCACTCGCTATACAGGAGTCTCTGTGATACACCCATCCGCGGGAGTGGTATAT	780						
Db	721	GACCACTCGCTATACAGGAGTCTCTGTGATACACCCATCCGCGGGAGTGGTATAT	780						
Qy	781	GAGTCTATCATGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840						
Db	781	GAGTCTATCATGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840						
Qy	841	TACAACATATGACAGAGCATTTGGACAGTGGCACCACCAACCTTCGTTTGGCCCAAGAAA	900						
Db	841	TACAACATATGACAGAGCATTTGGACAGTGGCACCACCAACCTTCGTTTGGCCCAAGAAA	900						
Qy	901	GTGTTTGAAGTGCAGTCAATCCATCAAGCAGCCTCCCTCCACGGAGAGTTCCCTGAT	960						
Db	901	GTGTTTGAAGTGCAGTCAATCCATCAAGCAGCCTCCCTCCACGGAGAGTTCCCTGAT	960						
Qy	961	GGTTTCTGGCTAGGAGAGCAGTGGTGTGCTGGCAAGCAGCCACCCCTTGGAAACATT	1020						
Db									

Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACACCCCTTGGAAACATT	1020						
Qy	1021	TTCCAGTCATCTCACTCTTAACTGGGTGAGTTACCAACAGTCTCTTCCGATCACC	1080						
Db	1021	TTCCAGTCATCTCACTCTTAACTGGGTGAGTTACCAACAGTCTCTTCCGATCACC	1080						
Qy	1081	ATCCTTCCGAGCAATACCTGCGGCCAGTGGAGATGTGCCACAGGACTGT	1140						
Db	1081	ATCCTTCCGAGCAATACCTGCGGCCAGTGGAGATGTGCCACAGGACTGT	1140						
Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGAGCTGTATCATGGAG	1200						
Db	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGAGCTGTATCATGGAG	1200						
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAACGAATGGCTTGTGTCAGGCTTGC	1260						
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAACGAATGGCTTGTGTCAGGCTTGC	1260						
Qy	1261	CATGTGCACATGATGTTTCAGACGGCAGCGGTGGAAGGCCCTTTTGTGCACCTTGGACATG	1320						
Db	1261	CATGTGCACATGATGTTTCAGACGGCAGCGGTGGAAGGCCCTTTTGTGCACCTTGGACATG	1320						
Qy	1321	GAGACTGTGGCTACAACTTCCACACAGATGAGTCAACCTCATGACCATAGACCTAT	1380						
Db	1321	GAGACTGTGGCTACAACTTCCACACAGATGAGTCAACCTCATGACCATAGACCTAT	1380						
Qy	1381	GTGATGCTGCCATCTCGGCCCTCTTTCATGCTGCACTCTGCTCATGCTGTCAGTGG	1440						
Db	1381	GTGATGCTGCCATCTCGGCCCTCTTTCATGCTGCACTCTGCTCATGCTGTCAGTGG	1440						
Qy	1441	CGCTGCCCTCGCTGCGCCAGCAGATGATGACTTTGCTGATGACATCTCCCTGCTG	1500						
Db	1441	CGCTGCCCTCGCTGCGCCAGCAGATGATGACTTTGCTGATGACATCTCCCTGCTG	1500						
Qy	1501	AAGTGAGAGGCCCATGGCAGAGATAGAGATTCCTCTGACACACCTCCGCTGGTCA	1560						
Db	1501	AAGTGAGAGGCCCATGGCAGAGATAGAGATTCCTCTGACACACCTCCGCTGGTCA	1560						
Qy	1561	CTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGCGCAGAGCCTCAGGACCTCC	1620						
Db	1561	CTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGCGCAGAGCCTCAGGACCTCC	1620						
Qy	1621	CCACCCACCAATGCTGCTGCTGAGAGAGAAAGCTGGCAAGTGGGTTCCAG	1680						
Db	1621	CCACCCACCAATGCTGCTGCTGAGAGAGAAAGCTGGCAAGTGGGTTCCAG	1680						
Qy	1681	GGACTGTACCTGTAGGAACAGAAAGAGAGAGAGGACCTCTGCTGGCGGAATACT	1740						
Db	1681	GGACTGTACCTGTAGGAACAGAAAGAGAGAGAGGACCTCTGCTGGCGGAATACT	1740						
Qy	1741	CTTGGTCACTCAAAATTAAGTCGGGAAATCTGCTGCTTGAATTCAGCCCTGAACCT	1800						
Db	1741	CTTGGTCACTCAAAATTAAGTCGGGAAATCTGCTGCTTGAATTCAGCCCTGAACCT	1800						
Qy	1801	TTGTCCACCATCTTTAAATTCCTCAACCCAAAGTATCTCTTTTCTTAGTTTCAGAA	1860						
Db	1801	TTGTCCACCATCTTTAAATTCCTCAACCCAAAGTATCTCTTTTCTTAGTTTCAGAA	1860						
Qy	1861	GTACTGCAATCACAGCAGGTTACCTTGGCTGTCTCCCTGTGCTGCTGCGGAGAG	1920						
Db	1861	GTACTGCAATCACAGCAGGTTACCTTGGCTGTCTCCCTGTGCTGCTGCGGAGAG	1920						
Qy	1921	AGACCAAGCTTGTTCCTCTGCTGCGGCAAGTACGTAGGAGGATGCACAGTTTCTATT	1980						
Db	1921	AGACCAAGCTTGTTCCTCTGCTGCGGCAAGTACGTAGGAGGATGCACAGTTTCTATT	1980						
Qy	1981	TGCTTTAGACAGGAGCTGTATTAACAAGCCTTAACATTTGCTGCAAGATTCCTCTTGA	2040						
Db	1981	TGCTTTAGACAGGAGCTGTATTAACAAGCCTTAACATTTGCTGCAAGATTCCTCTTGA	2040						
Qy	2041	ATTAATAAAAAAAAAAAAAAAAAAAAAA 2070							
Db	2041	ATTAATAAAAAAAAAAAAAAAAAAAAAA 2070							

Query Match	89.1%;	Score 1843.4;	DB 4;	Length 2370;
Best Local Similarity	98.8%;	Pred. No. 0;		
Matches 1867;	Conservative	0;	Mismatches 21;	Indels 1;

[illegible]

RESULT 7

RESUL /
US-09-548-372D-7

US-09-548-372D-7
: sequence 7: Application US/09548372D; Sequence 7, Application
: Patent No. 6470534

; Patent No. 6420534

; GENERAL INFORMATION:

APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER

1. TITLE OF INVENTION: THEREOF

FILE REFERENCE: 29915/6280I

FILE REFERENCE: 299TS/02601
CURRENT APPLICATION NUMBER: US/09/548,372D

;; CURRENT APPLICATION NUMBER: US/09/348,372
: CURRENT FILING DATE: 2000-04-12

; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: IIS 60/155,493

Query Match	75.0%	Score 1552.4	DB 4	Length 2043
Best Local Similarity	87.6%	Pred. No. 0		
Matches 1800	Conservative 0	Mismatches 241	Indels 13	Gaps 9
1	ATGCCCAAGCCCTCGCCTCGCTCTCTCTGTGGATGGCGGGAGTGTCTGCTGCCCCAC	60		
1	ATGCCCCAGCGCTGCACCTGGCTCTCTCTGTGGTGGGCTCGGAATGCTGCTGCCCCAG	60		
61	GGCACCCAGCAGCCGATCCGCTGCCCTTGGCGAGCGGCTTGGGGGGGCCCCCTCGGG	120		
61	GGAAACCATTCTGGCATCCGGCTGCCCTTCGCAGCGGCTTGGCAGGGCCACCCCTGGGC	120		
121	CTGGGCTGCCCGGAGACGGACGAGAGCCCGAGAGCCCGCGCGGAGGGGCGAGCTTT	180		
121	CTGAGGCTGCCCGGAGATGACGAGGAATCGGAGGAGCCTGGCCGAGAGGCAAGCTTT	180		
181	GTGGAGATGTGGAAACCTTGAGGGGCAAGTCGGGGAGGCTACTACGTGGAGATGACC	240		
181	GTGGAGATGTGNACACCTTGAGGGGAAAGTCCGCCAGGCTACTATGTGGAGATGACC	240		
241	GTGGGAGCCCCCGCAGAGCGCTCAACATCTCTGTGGATACAGGACGAGTAACCTTGA	300		
241	GTAGGAGCCCCCAGAGCGCTCAACATCTCTGTGGACACGGGAGTGTAGTAACCTTGA	300		
301	GTGGGTCTGCCCGCCACCCCTTCTGCATCGCTACTACAGAGGCGACTGTGCCAGACA	360		
301	GTGGGGCTGCCCGCACCCCTTCTGCATCGCTACTACAGAGGCGACTGTGCCAGACA	360		
361	TACCGGACCTCCGGAAGGTTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	420		
361	TATCGAGACCTCCGGAAGGTTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAA	420		
421	CTGGGCACGACCTGGTAAGCATCCCGCATGGCCCAACAGTCACTGTGCTGCCAACATT	480		
421	CTGGGCACGACCTGGTAGCATCCCTCATGGCCCAACAGTCACTGTGCTGCCAACATT	480		
481	CGTGCCATCACTGAATCAGACAAGTCTTTCATCAACGCTCCAACTGGGAGGCATCCGT	540		
481	CGTGCCATCACTGAATCGGACAAGTCTTTCATCAATGGTTCCAACTGGGAGGCATCTA	540		
541	GGGCTGCCCTATGCTGAGATTGCCAGGCGCTGACGACTCCCTGGAGCCCTTTCTTACCT	600		
541	GGGCTGCCCTATGCTGAGATTGCCAGGCCGACGACTCTTTGGAGCCCTTCTTGGACTCC	600		
601	CTGGTAAGCAGACCCAGTTCCCAACCTCTTCTCCCTGCAACCTTTGTGGTCTGGCTTC	660		
601	CTGGTAAGCAGACCCACATCCCAACATCTTTTCCCTGCAAGTCTGTGGGCTGGCTTC	660		
661	CCCTCAACAGTCTGAAGTCTGGCCCTCTCTCGGAGGGACATCATATTGGAGGTATC	720		
661	CCCTCAACAGACCGAGGACCTGGCCCTCTCGGAGGGAGCATGATCATTTGGTGGTATC	720		
721	GACCACTCGGTACACAGGCGAGTCTCTGGTATACACCCATCCCGCGGAGTGGTATTAT	780		
721	GACCACTCGGTATACAGGCGAGTCTCTGGTATACACCCATCCCGCGGAGTGGTATTAT	780		
781	GAGGTATCATATTGTGCGGGTGGAGATCAATGGACGAGTATCGAAATGGACTGCAAGAG	840		

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-548-372D-31

Query Match 65.7%; Score 1359; DB 4; Length 1380;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCCCAAGCCCTCCCTGGCTGCTGTGGATGGCGCGGAGTGTGCTGCCCCAC	60
DB	1	ATGGCCCAAGCCCTCCCTGGCTGCTGTGGATGGCGCGGAGTGTGCTGCCCCAC	60
QY	61	GGCACCAGCAGCGGATCCGGTGCCTTGGCGAGCGGCGGCCCGCCCTGGGG	120
DB	61	GGCACCAGCAGCGGATCCGGTGCCTTGGCGAGCGGCGGCCCGCCCTGGGG	120
QY	121	CTGGGGTCCCGCGGAGACCGACGAAGAGCCGAGGAGCCGCGCGGAGGGCAGCTTT	180
DB	121	CTGGGGTCCCGCGGAGACCGACGAAGAGCCGAGGAGCCGCGCGGAGGGCAGCTTT	180
QY	181	GTGGAGATGGTGGAACCTGAGGGGCAAGTGGGGGAGGCTACTAGTGGAGATGACC	240
DB	181	GTGGAGATGGTGGAACCTGAGGGGCAAGTGGGGGAGGCTACTAGTGGAGATGACC	240
QY	241	GTGGCAGCCCCCGCAGACGCTCAACATCTCTGTGTGATACAGGAGCAGTAACATTGCA	300
DB	241	GTGGCAGCCCCCGCAGACGCTCAACATCTCTGTGTGATACAGGAGCAGTAACATTGCA	300
QY	301	GTGGGTGTGCCCCCACCCTTCTGCTGCTACTACAGAGGCGAGTGTCCAGCACA	360
DB	301	GTGGGTGTGCCCCCACCCTTCTGCTGCTACTACAGAGGCGAGTGTCCAGCACA	360
QY	361	TACCGGAGCTCCGGAAGGTTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGAG	420
DB	361	TACCGGAGCTCCGGAAGGTTGTATGTGCCCTACACCCAGGCGAAGTGGGAAGGGAG	420
QY	421	CTGGCAGCGAGCTGTGAAGCATCCCGATGCCCGCAACGTCACCTGTGCGTCCCAACATT	480
DB	421	CTGGCAGCGAGCTGTGAAGCATCCCGATGCCCGCAACGTCACCTGTGCGTCCCAACATT	480
QY	481	GCTGCCATCACTGAATACAGAAAGTTCTTCAACAGCGCTCCCACTGGGAAGGCATCCTG	540
DB	481	GCTGCCATCACTGAATACAGAAAGTTCTTCAACAGCGCTCCCACTGGGAAGGCATCCTG	540
QY	541	GGGCTGGCCTATGCTGAGATGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTCACTCT	600
DB	541	GGGCTGGCCTATGCTGAGATGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTCACTCT	600
QY	601	CTGGTAAAGCAGACCCAGCTTCCCAACCTTCTCTCCCTGACCTTTGTGGTCTGGCTTC	660
DB	601	CTGGTAAAGCAGACCCAGCTTCCCAACCTTCTCTCCCTGACCTTTGTGGTCTGGCTTC	660
QY	661	CCCCTCAACAGTCTGAAGTGTGCGCTCTGTGCGGAGGAGCATGATCATTTGGAGTATC	720
DB	661	CCCCTCAACAGTCTGAAGTGTGCGCTCTGTGCGGAGGAGCATGATCATTTGGAGTATC	720

RESULT 12

US-09-548-367D-31

; Sequence 31, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

; FILE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 1380

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-548-367D-31

Db 282 GGGTCTGCCCGCCACCCCTTCCCTGTCATCGTACTACAGAGGAGCTGTCCAGCACATA 341
QY 363 CCGGACCTCCGGAGGCTGTATGTCCCTACACCCAGGCAAGTGGAGGGAGCT 422
Db 342 CCGGACCTCCGGAGGCTGTATGTCCCTACACCCAGGCAAGTGGAGGGAGCT 401
QY 423 GGGCAGCAGCTGTGAAGTATCCCGGAGGCTGTCCCTACCTGTGCGTGCACATTCG 482
Db 402 GGGCAGCAGCTGTGAAGTATCCCGGAGGCTGTCCCTACCTGTGCGTGCACATTCG 461
QY 483 TGCCATCACTCAATCAGACAGTTCCTCATCAAGGGCTCCCACTGGGAAGGATCCTGGG 542
Db 462 TGCCATCACTCAATCAGACAGTTCCTCATCAAGGGCTCCCACTGGGAAGGATCCTGGG 521
QY 543 GCTGCTATGCTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 602
Db 522 GCTGCTATGCTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 581
QY 603 GGTAAAGCAGACCCAGCTTCCCAAGCTTCTTCCCTGCACCTTTTGTGTGCTGGCTTCCC 662
Db 582 GGTAAAGCAGACCCAGCTTCCCAAGCTTCTTCCCTGCACCTTTTGTGTGCTGGCTTCCC 641
QY 663 CCTCAACCACTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 722
Db 642 CCTCAACCACTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 701
QY 723 CCATCTGCTGTACAGGAGCTGTCTGTGTATACCCCTTCCCGGGAGTGGTATATGA 782
Db 702 CCATCTGCTGTACAGGAGCTGTCTGTGTATACCCCTTCCCGGGAGTGGTATATGA 761
QY 783 GGTATCATATGTGGGGTGGAGTCAATGAGAGGATCTGAAATGGAGTCAAGAGGAGTA 842
Db 762 GGTATCATATGTGGGGTGGAGTCAATGAGAGGATCTGAAATGGAGTCAAGAGGAGTA 821
QY 843 CAATATACAGAGGATTTGGAGAGTGGACAGTGGACACCAACCTTGTGTTGCCAAGAAAGT 902
Db 822 CAATATACAGAGGATTTGGAGAGTGGACAGTGGACACCAACCTTGTGTTGCCAAGAAAGT 881
QY 903 GTTTGAAGCTGAGTCAATCCATCAAGGAGGCTTCCCTCCAGGAGAGTTCCTGTATGG 962
Db 882 GTTTGAAGCTGAGTCAATCCATCAAGGAGGCTTCCCTCCAGGAGAGTTCCTGTATGG 941
QY 963 TTTCTGGCTAGGAGAGGAGTGTGTGTGTGCAAGGAGGACACCCCTTGGAAATTTT 1022
Db 942 TTTCTGGCTAGGAGAGGAGTGTGTGTGTGCAAGGAGGACACCCCTTGGAAATTTT 1001
QY 1023 CCCAGTCACTCACTTACCTTAATGGGTGAGGTTACCAACAGTCTTCCGCTACCAT 1082
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QY 1083 CTTTCCGAGCAATACCTTCCGCGGAGTGGAGAGTGGCCACGTCGCCAAGACGACTGTTA 1142
Db 1062 CTTTCCGAGCAATACCTTCCGCGGAGTGGAGAGTGGCCACGTCGCCAAGACGACTGTTA 1121
QY 1143 CAAGTTTCCATCTCACAGTCAATCCAGGGGAGTGTATGGAGTGTATATCATGGAGG 1202
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QY 1203 CTTCTACGTTGTCTTTGATCGGGCCGAAACGAATTCGCTGTGCTGCTGAGGCTTGGCA 1262
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QY 1263 TGTGCACGATGAGTTCAGGAGGAGGAGGCTTGGAGGCTTTTGTGACCTTGGACATGGA 1322
Db 1242 TGTGCACGATGAGTTCAGGAGGAGGAGGCTTGGAGGCTTTTGTGACCTTGGACATGGA 1301
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RESULT 14

US-09-548-367D-21
; Sequence 21, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-21

Query Match 62.7%; Score 1297; DB 4; Length 1341;
Best Local Similarity 100.0%; Pred. No. 9,9e-310;

Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 CACCCAGCAGCGATCCCGCTGCCCTCGCAGCGGCTGGGGGCGCCCGCCCTGGGGCT 122
Db 42 CACCCAGCAGCGATCCCGCTGCCCTCGCAGCGGCTGGGGGCGCCCGCCCTGGGGCT 101
QY 123 GCGCTGCCCGGGAGACCGGAGAGAGCCCGAGAGAGCCCGGAGAGCCCGGAGGAGCTTTGT 182
Db 102 GCGCTGCCCGGGAGACCGGAGAGAGCCCGGAGAGCCCGGAGGAGCTTTGT 161
QY 183 GGAGATGTGGACAACCTTGAGGGCAAGTCGGGGGAGGCTACTACGTGGAGATCACCGT 242
Db 162 GGAGATGTGGACAACCTTGAGGGCAAGTCGGGGGAGGCTACTACGTGGAGATCACCGT 221
QY 243 GGGAGCCCCCGCAGAGCGCTCAACATCCTGGTGGATACAGGACAGCTAACTTTGCGAGT 302
Db 222 GGGAGCCCCCGCAGAGCGCTCAACATCCTGGTGGATACAGGACAGCTAACTTTGCGAGT 281
QY 303 GGGTCTGCCCGCCACCCCTTCCCTGCTATCTACAGAGGAGCTTCCAGACATA 362
Db 282 GGGTCTGCCCGCCACCCCTTCCCTGCTATCTACAGAGGAGCTTCCAGACATA 341
QY 363 CCGGACCTCCGGAGGCTGTATGTGCCCTTACACCCAGGCAAGTGGGAAGGAGCT 422
Db 342 CCGGACCTCCGGAGGCTGTATGTGCCCTTACACCCAGGCAAGTGGGAAGGAGCT 401
QY 423 GGGCAGCAGCTGTGAAGTATCCCGGAGGCTGTCCCTACCTGTGCGTGCACATTCG 482
Db 402 GGGCAGCAGCTGTGAAGTATCCCGGAGGCTGTCCCTACCTGTGCGTGCACATTCG 461
QY 483 TGCCATCACTCAATCAGACAGTTCCTCATCAAGGGCTCCCACTGGGAAGGATCCTGGG 542
Db 462 TGCCATCACTCAATCAGACAGTTCCTCATCAAGGGCTCCCACTGGGAAGGATCCTGGG 521
QY 543 GCTGCTATGCTGAGATTGGCAGGCTGAGACCTTCCCTGGAGGCTTTCTTTGACTCTCT 602
Db 522 GCTGCTATGCTGAGATTGGCAGGCTGAGACCTTCCCTGGAGGCTTTCTTTGACTCTCT 581
QY 603 GGTAAAGCAGACCCAGCTTCCCAAGCTTCTTCCCTGCACCTTTTGTGTGCTGGCTTCCC 662
Db 582 GGTAAAGCAGACCCAGCTTCCCAAGCTTCTTCCCTGCACCTTTTGTGTGCTGGCTTCCC 641
QY 663 CCTCAACCACTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 722
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[illegible]

RESULT 15

US-09-548-372D-23
Sequence 23, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548, 372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 1380
TYPE: DNA
ORGANISM: Homo sapiens
US-09-548-372D-23

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Qy	1203	CTTCTACGTTGTCTTTTGATCGGCGCCGAAACAAATTTGGCTTGTGTACGCGCTTGGCCA	1262
Db	1221	CTTCTACGTTGTCTTTTGATCGGCGCCGAAACAAATTTGGCTTGTGTACGCGCTTGGCCA	1280
Qy	1263	TGTGTCAGGATGAGCTTCAGNACGCGAGGGTGGGAAGGCCCTTTTGTGCACCTTGACACATGA	1322
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Qy	1323	AGACTGTGGCTACAACATTCACACAGACAGATGAGTCA	1359
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 Job time : 104 secs

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OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:12 ; Search time 5392 Seconds
(without alignments)
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Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgcctg.....aaaaaaaaaaaaaaaaaaaaa 2070

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Searched: 2054640 seqs, 14551402878 residues
11 number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	2062	99.6	2526	9	AF190725	AF190725 Homo sapi
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6	2040	98.6	5814	9	AB032975	AB032975 Homo sapi
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8	2032	98.2	2541	6	AX002655	AX002655 Sequence
9	2032	98.2	2541	6	E50816	E50816 Aspartate p
10	2010	97.1	3252	6	AX062111	AX062111 Sequence
11	2010	97.1	3252	6	AX063201	AX063201 Sequence
12	2010	97.1	3252	6	AX472368	AX472368 Sequence
13	2010	97.1	3252	9	AF200193	AF200193 Homo sapi
14	1894.2	91.5	5757	6	AX364933	AX364933 Sequence
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17	1843.4	89.1	2370	6	AR178470	AR178470 Sequence
18	1843.4	89.1	2370	6	AX002657	AX002657 Sequence
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C 44	790.8	38.2	149843	9	AP000892	AP000892 Homo sapi
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DEFINITION	AX105385					
ACCESSION	AX105385					
VERSION	AX105385.1	GI:13921511				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 2070)					
AUTHORS	Gurney, M. and Blenkowski, M.J.					
TITLE	Alzheimer's disease secretase, app substrates therefor, and uses therefor					

JOURNAL
Patent: WO 0123533-A 3 05-APR-2001;
pharmacia & Upjohn Company (US)

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
/ab_vref="taxon:9606"
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Query Match	100.0%;	Score 2070;	DB 6;	Length 2070;
Best Local Similarity	100.0%;	Pred. No. 0;		
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DB	1	ATGCCCAAGCCCTGCCTGCCTCTCTCTGTGTGGATGGCGCGGAGTGTCTGCTTGCAC	60	
QY	61	GGCACCAGCAGCAGCCTCCGCTGCCTCTGCAGCGGCTTGGGGGGGCGCCCTGGGG	120	
DB	61	GGCACCAGCAGCAGCCTCCGCTGCCTCTGCAGCGGCTTGGGGGGGCGCCCTGGGG	120	
QY	121	CTGGGCTTGCCTCCGGGAGCAGCAAGAGCCCGAGAGCCCGGGCGGAGGGGCGAGCTTT	180	
DB	121	CTGGGCTTGCCTCCGGGAGCAGCAAGAGCCCGAGAGCCCGGGCGGAGGGGCGAGCTTT	180	
QY	181	GTGGAGATGGTGGACAACTCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGAGATGACC	240	
DB	181	GTGGAGATGGTGGACAACTCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGAGATGACC	240	
QY	241	GTGGCAGCCCCCGCAGACGCTCAACATCTCTGGTGGATACAGGCAGCAGTAACTTTGCA	300	
DB	241	GTGGCAGCCCCCGCAGACGCTCAACATCTCTGGTGGATACAGGCAGCAGTAACTTTGCA	300	
QY	301	GTGGGTGTGCCCCCAGCCCTTCTGTGATCGCTACTACAGAGGCAGCTGTCCACGACA	360	
DB	301	GTGGGTGTGCCCCCAGCCCTTCTGTGATCGCTACTACAGAGGCAGCTGTCCACGACA	360	
QY	361	TACCGGGACTCTCGGAAGGCTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420	
DB	361	TACCGGGACTCTCGGAAGGCTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420	
QY	421	CTGGGCACCGACTGTGTAAAGATFCCCCCATGGCCCCAAGCTCACTGTGGTGGCCCAACAT	480	
DB	421	CTGGGCACCGACTGTGTAAAGATFCCCCCATGGCCCCAAGCTCACTGTGGTGGCCCAACAT	480	
QY	481	GGTGGCATCACTCAATCAGACAAAGTCTTTCATCAAGGGCTCCAACTGGGAAGGCATCCTG	540	
DB	481	GGTGGCATCACTCAATCAGACAAAGTCTTTCATCAAGGGCTCCAACTGGGAAGGCATCCTG	540	
QY	541	GGGCTGGCCCTATGCTGAGATGGCAGGCTTGAGACTCCCTGGAGCCCTTCTTGTGACTCT	600	
DB	541	GGGCTGGCCCTATGCTGAGATGGCAGGCTTGAGACTCCCTGGAGCCCTTCTTGTGACTCT	600	
QY	601	CTGGTAAAGCAGACCCACGTTCCCAACTCTTCTCCCTGCACCTTTGTGTGCTGGCTTC	660	
DB	601	CTGGTAAAGCAGACCCACGTTCCCAACTCTTCTCCCTGCACCTTTGTGTGCTGGCTTC	660	
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QY	721	GACCACTGCTGTACACAGGAGCTCTGGTGTATACCCATCCGGCGGAGCTGTGTTAT	780	
DB	721	GACCACTGCTGTATACAGGAGCTCTCTGGTGTATACCCATCCGGCGGAGCTGTGTTAT	780	
QY	781	GAGTCTCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGAG	840	
DB	781	GAGTCTCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGAG	840	
QY	841	TACAACTATGACAGAGCATTTGTGGACAGTGGCACCACCACTTCGTTTGGCCCAAGAAA	900	
DB	841	TACAACTATGACAGAGCATTTGTGGACAGTGGCACCACCACTTCGTTTGGCCCAAGAAA	900	

Qy	901	GTGTTTGAAGCTGCAGTCAAAATCCATCAATGACGACGCTCTCCACGGAGAAGTTCCCTGAT	960
Db	901		
Qy	901	GTGTTTGAAGCTGCAGTCAAAATCCATCAATGACGACGCTCTCCACGGAGAAGTTCCCTGAT	960
Db	901		
Qy	961	GGTTTCTGGCTAGGAGACGACTGTGTGCTGGCAAGCAGGACACACCCCTTGGAAACATT	1020
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Qy	1021	TTCCAGTCAATCTCACTAATATGGGTGAGGTTACCAACCACTCTCCCGCATCAC	1080
Db	1021		
Qy	1021	TTCCAGTCAATCTCACTAATATGGGTGAGGTTACCAACCACTCTCCCGCATCAC	1080
Db	1021		
Qy	1081	ATCCTTCCGCGAGCAATACCTGCGGCCAGTGAAGATGTGGCCACGTCCTCCAAAGACACTGT	1140
Db	1081		
Qy	1081	ATCCTTCCGCGAGCAATACCTGCGGCCAGTGAAGATGTGGCCACGTCCTCCAAAGACACTGT	1140
Db	1081		
Qy	1141	TACAAAGTTGGCAATCTACAGTCAATCCACGGGCACACTGTTATCGGAGCTCTTATCATGGAG	1200
Db	1141		
Qy	1201	GCCTTCTAGTTGTCTTTGATCGGCCCGCCGAAACGAAATTTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201		
Qy	1201	GCCTTCTAGTTGTCTTTGATCGGCCCGCCGAAACGAAATTTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201		
Qy	1261	CATGTGCAGATGAGTTCAAGCAGCGGCTGGGAAGGCCCTTTTCTCACTTTGGACATG	1320
Db	1261		
Qy	1261	CATGTGCAGATGAGTTCAAGCAGCGGCTGGGAAGGCCCTTTTCTCACTTTGGACATG	1320
Db	1261		
Qy	1321	GAAGACTTGGCTACAAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGGCTAT	1380
Db	1321		
Qy	1321	GAAGACTTGGCTACAAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGGCTAT	1380
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Db	1441		
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Qy	1561	CTTTGGTCAAGTAGGAGACACAGATGGACCTGTGGCCAGACACCTCAGGACCCCTCC	1620
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Qy	1561	CTTTGGTCAAGTAGGAGACACAGATGGACCTGTGGCCAGACACCTCAGGACCCCTCC	1620
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Qy	1681	GGACTGTAACCTGTAGGAACAGAAAGAGAGACACTGTGCTGGCGGGAATACT	1740
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Qy	1261	CATGTGCACCATGAGTTTCAGAGCGCAGCGGTGGAAGGCCCTTTTGTCACTTTGGACATG	1320
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Qy	1321	GAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
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Qy	1441	CGCTGCGCTCGCTGCGCTGCGCCAGCAGCATGATGCTTCTGATGACATCTCCCTGCTG	1500
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Qy	1621	CCACCCACAAATGCCCTCTGCCCTTGATGGAGAAGGAAAAGSGCTGGAAAGTGGGTGCCAG	1680
Db	1621	CCACCCACAAATGCCCTCTGCCCTTGATGGAGAAGGAAAAGSGCTGGAAAGTGGGTGCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAACAGAAAAGAGAAAGAACGACATCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAACAGAAAAGAGAAAGAACGACATCTGCTGGCGGGAATACT	1740
Qy	1741	CTTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCTGCTTTGAAACTTTCAGCCCTGAACCT	1800
Db	1741	CTTTGGTCACCTCAAAATTTAAGTCGGGAAATTCCTGCTGCTTTGAAACTTTCAGCCCTGAACCT	1800
Qy	1801	TTGTGCCACCATCTCTTTAAATTCCTCAACCCCAAGATATCTCTCTTTCTTAGTTTTCAGAA	1860
Db	1801	TTGTGCCACCATCTCTTTAAATTCCTCAACCCCAAGATATCTCTCTTTCTTAGTTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGAGGTTACCTTTGGCGTGTGCCCTGTGGTATCCCTTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGAGGTTACCTTTGGCGTGTGCCCTGTGGTATCCCTTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTCCTGCTGCCCAAGTCTAGTAGGAGAGGATGCACAGTTTGTCTATT	1980
Db	1921	AGACCAAGCTTGTTCCTGCTGCCCAAGTCTAGTAGGAGAGGATGCACAGTTTGTCTATT	1980
Qy	1981	TGCTTTAGACACAGGACTGTATAACAAGCCCTAACTTGGTGGCAAGATTGGCTCTGTGA	2040
Db	1981	TGCTTTAGACACAGGACTGTATAACAAGCCCTAACTTGGTGGCAAGATTGGCTCTGTGA	2040

QY	2041	ATTAAAAA	2070
DB	2041	ATTTAAAAA	2070
RESULT 4			
LOCUS	AF190725	2526 bp	linear
DEFINITION	Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.		
ACCESSION	AF190725		
VERSION	AF190725.1	GI:6118538	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 2526) Vassar, R., Bennett, B.D., Babu-Khan, S., Kahn, S., Mendiaz, E.A., Denis, P., Teplow, D.B., Ross, S., Amarante, P., Loeloff, R., Luo, Y., Fisher, S., Fuller, J., Edenson, S., Lile, J., Jarosinski, M.A., Biere, A.L., Curran, E., Burgess, T., Louis, J.C., Collins, F., Treanor, J., Rogers, G. and Citron, M.		
TITLE	Beta-secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE		
JOURNAL	Science 286 (5440), 735-741 (1999)		
MEDLINE	20002972		
PUBMED	10531052		
REFERENCE	2 (bases 1 to 2526) Bennett, B.D., Vassar, R. and Citron, M.		
AUTHORS	Direct Submission		
TITLE	Submitted (29-SEP-1999) Neuroscience, Amgen Inc., One Amgen Center		
JOURNAL	Dr., Thousand Oaks, CA 91320-1799, USA		
FEATURES	Location/Qualifiers 1..2526 /organism="Homo sapiens" /db_xref="taxon:9606" 2..2526 /gene="BACE" 454..1959 /gene="BACE" /codon_start=1 /product="beta-site APP cleaving enzyme" /protein_id="AAF04142.1" /db_xref="GI:6118539" /translation="MAQALPWLMLMGAGVLPAGHQHGRIRLPLRSLGGAGPILGLRLP RATDEEPEPRGRGSFVEMVDNRKSGQGYVETMGVSPPTLNLTVDTGSSNFVAG AAPPFHRYHQRLSTDLRKGVVPTQGWGELGTLVSTVPHGPNVPRANI AAITPESDFVINGSGWIIIGLGAETARPDSDLPEFDSLKQTHVNLFSIQLCGA GFLPNSEVLAYSGGSMIIIGDHSLTGSLWYTPPRREWYEVIIIVELINEQDLKA DCKEYNDKSVDSGTNLRPKPFVFAAVKSIKAASSTKFPDGGFWLGEQLVCWQAG TTPNWIIPVLSLYLMGVEITNOSRITILPOOYLRPVEDVATSDQDCYKFAISQSTGT VMGAVIMEGVYVDFARKRGFAVSACHVHDEFRTAAVEGPEVTLMDGCGYNIPQT DESTPLMTIAYVMAICALEFMLPLCLMVCQWRCLRLRQHQHDDFADDSILLK"		
BASE COUNT	534 a	781 c	715 g 496 t
ORIGIN			
Query Match	99.6%	Score 2062;	DB 9; Length 2526;
Best Local Similarity	99.8%	Pred. No. 0;	
Matches 2065;	Conservative 0;	Mismatches 5;	Indels 0; Gaps 0;
QY	1	ATGCCCCAAGCCCTGCCTGGCTCCTGCTGGATGGCGCGGAGTGTGCTGCCCTGCCAC	60
DB	454	ATGCCCCAAGCCCTGCCTGGCTCCTGCTGGATGGCGCGGAGTGTGCTGCCCTGCCAC	513
QY	61	GGCACCAGCAGCGCATCGGCTGCCCTGCAGCGCGCTGGGGGCGCCCCCTGGGG	120
DB	514	GGCACCAGCAGCGCATCGGCTGCCCTGCAGCGCGCTGGGGGCGCCCCCTGGGG	573
QY	121	CTCGGGTGTCCCCGGGAGACCGACGAGAGCCCGAGAGCCCGCGGAGGCGACGCTTT	180
DB	574	CTCGGGTGTCCCCGGGAGACCGACGAGAGCCCGAGAGCCCGCGGAGGCGACGCTTT	633

QY	181	GTG	GAG	ATGGTGG	ACAAACCTGAGGCGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC	240
DB	634	GTG	GAG	ATGGTGG	ACAAACCTGAGGCGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC	693
QY	241	GTGGC	AGCCCCC	CGACGCTCAACATCCTGTGTGATACAGCGACGAGTAACATTGCA	300	
DB	694	GTGGC	AGCCCCC	CGACGCTCAACATCCTGTGTGATACAGCGACGAGTAACATTGCA	753	
QY	301	GTGGTGTG	CCCCCCCC	CCCTTCCTGCATCGCTACTACCAGAGGCAAGCTGTCCAGCAC	360	
DB	754	GTGGTGTG	CCCCCCCC	CCCTTCCTGCATCGCTACTACCAGAGGCAAGCTGTCCAGCAC	813	
QY	361	TACCGG	AGCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	420		
DB	814	TACCGG	AGCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	873		
QY	421	CTGGG	CACGACCTGGTAAGCATCCCCATGGCCCCCAACGTCACCTGTGCGGTGCCAACATT	480		
DB	874	CTGGG	CACGACCTGGTAAGCATCCCCATGGCCCCCAACGTCACCTGTGCGGTGCCAACATT	933		
QY	481	GCCTGCC	ATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540		
DB	934	GCCTGCC	ATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	993		
QY	541	GGGCTG	GCCTATGCTGAGATTGGCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600		
DB	994	GGGCTG	GCCTATGCTGAGATTGGCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	1053		
QY	601	CTGTAA	AGCAGACCCACACGTTCCCAACCTTCTCTCCCTGCACCTTTGTGGTGGGCTC	660		
DB	1054	CTGTAA	AGCAGACCCACACGTTCCCAACCTTCTCTCCCTGCACCTTTGTGGTGGGCTC	1113		
QY	661	CCCC	TCAACGAGTCTGAAGTGTGGCCTCTGTGGAGGAGCATCATTTGGAGGTATC	720		
DB	1114	CCCC	TCAACGAGTCTGAAGTGTGGCCTCTGTGGAGGAGCATCATTTGGAGGTATC	1173		
QY	721	GACCA	CTCGTGACACGACGCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780		
DB	1174	GACCA	CTCGTGACACGACGCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	1233		
QY	781	GAGGT	CACTCATPTGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACATCGAAGGAG	840		
DB	1234	GAGGT	CACTCATPTGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGACATCGAAGGAG	1293		
QY	841	TACA	ACTATGACAGACGATTTGGACAGTGGCACCAACCTTCGTTTGGCCCAAGAAA	900		
DB	1294	TACA	ACTATGACAGACGATTTGGACAGTGGCACCAACCTTCGTTTGGCCCAAGAAA	1353		
QY	901	GTGTTT	GAGCTGCAGTCAAAATCATCAAGGACGCTCTCCACGGAGAAGTTCCTGAT	960		
DB	1354	GTGTTT	GAGCTGCAGTCAAAATCATCAAGGACGCTCTCCACGGAGAAGTTCCTGAT	1413		
QY	961	GGTTT	CTGGTAGGAGACGCTGTGTGCGCAAGCAGGCAACCCCTTGGAAACATT	1020		
DB	1414	GGTTT	CTGGTAGGAGACGCTGTGTGCGCAAGCAGGCAACCCCTTGGAAACATT	1473		
QY	1021	TTCC	CAGTCATCTCACTACTACCTAATGGGTGAGGTTACCAACCAAGTCCCTCCGCATCAC	1080		
DB	1474	TTCC	CAGTCATCTCACTACTAATGGGTGAGGTTACCAACCAAGTCCCTCCGCATCAC	1533		
QY	1081	ATCC	TTCCGCGACGATACCTGGGCGCAGTGGAAAGATGTGGCAGCTCCCAAGACGACTGT	1140		
DB	1534	ATCC	TTCCGCGACGATACCTGGGCGCAGTGGAAAGATGTGGCAGCTCCCAAGACGACTGT	1593		
QY	1141	TACA	AGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGAGGTGTTATCATGGAG	1200		
DB	1594	TACA	AGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGAGGTGTTATCATGGAG	1653		
QY	1201	GGCT	TTACAGTGTCTTTGATCGGGCCGGAACGAATTCGCTTGCTGTCAGCGCTTGC	1260		
DB	1654	GGCT	TTACAGTGTCTTTGATCGGGCCGGAACGAATTCGCTTGCTGTCAGCGCTTGC	1713		

QY	1261	CATGTGCAGCATGAGTT	CAGGACGCGACGGT	TGGAAGGCCCTTT	TGTACCTTGGACATG	1320
Db	1714	CATGTGCAGCATGAGTT	CAGGACGCGACGGT	TGGAAGGCCCTTT	TGTACCTTGGACATG	1773
QY	1321	GAAGACTGTGGGTACAA	CAATTCACAGACAGAT	GAGTCAACCCCTCATG	ACCATAGCCTAT	1380
Db	1774	GAAGACTGTGGGTACAA	CAATTCACAGACAGAT	GAGTCAACCCCTCATG	ACCATAGCCTAT	1833
QY	1381	GTCAATGGCTGCCATCG	CGCCCTTTCATGCTGC	CACTCTGCCTCATGGT	GTGTCAAGTGG	1440
Db	1834	GTCAATGGCTGCCATCG	CGCCCTTTCATGCTGC	CACTCTGCCTCATGGT	GTGTCAAGTGG	1893
QY	1441	CGTGTGCTCCGCTGCT	CGCCAGCAGCATGAT	GATGACTTTGCTGAT	GACATCTCCCTGCTG	1500
Db	1894	CGTGTGCTCCGCTGCT	CGCCAGCAGCATGAT	GATGACTTTGCTGAT	GACATCTCCCTGCTG	1953
QY	1501	AAGTGAGGAGCCCATG	GGCGAGAAATAGAGAT	TCCCTTGGACCACACT	CCGTGGTTTCA	1560
Db	1954	AAGTGAGGAGCCCATG	GGCGAGAAATAGAGAT	TCCCTTGGACCACACT	CCGTGGTTTCA	2013
QY	1561	CTTTGGTCACAAGT	TAGGAGACAGATGG	CACCTGTGGCCAGAC	CTCAGACCCCTCC	1620
Db	2014	CTTTGGTCACAAGT	TAGGAGACAGATGG	CACCTGTGGCCAGAC	CTCAGACCCCTCC	2073
QY	1621	CCACCCACCAATGCC	CTCTGCCCTTGATG	GAGAGAAAGGCTG	GCAAGGTGGTTCAG	1680
Db	2074	CCACCCACCAATGCC	CTCTGCCCTTGATG	GAGAGAGAAAGGCT	GCAAGGTGGTTCAG	2133
QY	1681	GGACTGTACCTGTAG	GAACACAGAAAGAG	AAGACACTCTCTCT	CTGGCGGATACT	1740
Db	2134	GGACTGTACCTGTAG	GAACACAGAAAGAG	AAGACACTCTCTCT	CTGGCGGATACT	2193
QY	1741	CTTGTGTACCTCAAA	TTTAAGTCGGGAAAT	CTGCTGTTGAAACT	TCAGCCCTGAACCT	1800
Db	2194	CTTGTGTACCTCAAA	TTTAAGTCGGGAAAT	CTGCTGTTGAAACT	TCAGCCCTGAACCT	2253
QY	1801	TTGTCCACCATTCCT	TTTAAATTCCTCAAC	CCCAAGTATCTCT	CTTTTCTAGTTTCAG	1860
Db	2254	TTGTCCACCATTCCT	TTTAAATTCCTCAAC	CCCAAGTATCTCT	CTTTTCTAGTTTCAG	2313
QY	1861	GTACTGGCATCACG	CAGATTACCTTGGCG	TGTCTCCCTGTGTAC	CTCCCTGGCCAGAGA	1920
Db	2314	GTACTGGCATCACG	CAGATTACCTTGGCG	TGTGTCTCCCTGTGT	ACCTGGCCAGAGA	2373
QY	1921	AGACCAAGCTCTTT	CCCTGCTGGCCAA	AGTCTAGTAGGAGG	ATGCACAGTTTGCTATT	1980
Db	2374	AGACCAAGCTCTTT	CCCTGCTGGCCAA	AGTCTAGTAGGAGG	ATGCACAGTTTGCTATT	2433
QY	1981	TGCTTTTAGAGAC	AGGGACTGTATAACA	AGCCCTACACTTGGT	CAAGATTGCCTCTTGA	2040
Db	2434	TGCTTTTAGAGAC	AGGGACTGTATAACA	AGCCCTACACTTGGT	CAAGATTGCCTCTTGA	2493
QY	2041	ATTAAAAA	AAAAAAAAAAAAAAAA	AAAAAAAA	2070	
Db	2494	ATTAAAAA	AAAAAAAAAA	AACTAGAAAA	2523	
RESULT 5						
AF201468			5878 bp	mRNA	linear	PRI 19-DEC-1999
LOCUS						

db	1955	AAGTGAGGAGGCCCATGGCGAAGATAGAGATTCCCTGTGACACACACTCCGTGGTTCA	2014
db	1561	CTTTGGTCAAGTAGAGACACAGATGGCACTGTGCGCAGAGACACTCAGGACCCCTCC	1620
db	2015	CTTTGGTCAAGTAGAGACACAGATGGCACTGTGCGCAGAGACACTCAGGACCCCTCC	2074
db	1621	CCAGCCACCAATGCCTCTGCTTGTATGGGAAGAAAGGCTGCGCAAGTGGGTTCAG	1680
db	2075	CCAGCCACCAATGCCTCTGCTTGTATGGGAAGAAAGGCTGCGCAAGTGGGTTCAG	2134
db	1681	GGACTGTACCTGTAGGAACAAGAAAGAGAGAGACACTCGCTGGCGGGAATACT	1740
db	2135	GGACTGTACCTGTAGGAACAAGAAAGAGAGAGACACTCGCTGGCGGGAATACT	2194
db	1741	CTTGTCACCTCAAAATTTAAGTCGGGAATTTCTGCTGTGAAACTTCAGCCCTGAACT	1800
db	2195	CTTGTCACCTCAAAATTTAAGTCGGGAATTTCTGCTGTGAAACTTCAGCCCTGAACT	2254
db	1801	TTTGCCACCATTCCTTTAAATTTCTCCAAACCCAAAGATTTCTTTCTTAGTTTCAGAA	1860
db	2255	TTTGCCACCATTCCTTTAAATTTCTCCAAACCCAAAGATTTCTTTCTTAGTTTCAGAA	2314
db	1861	GTACTGGCATCACACGCAAGTTACCTTGGCGTGTGCTGCTGGTACCTGCGCAGAGAAG	1920
db	2315	GTACTGGCATCACACGCAAGTTACCTTGGCGTGTGCTGCTGGTACCTGCGCAGAGAAG	2374
db	1921	AGACCAAGCTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTGCATT	1980
db	2375	AGACCAAGCTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTGCATT	2434
db	1981	TGCTTTAGACAGGAGCTGTATAACAGCCCTAACATTGGTGCRAAGATTGCTCTTGA	2040
db	2435	TGCTTTAGACAGGAGCTGTATAACAGCCCTAACATTGGTGCRAAGATTGCTCTTGA	2494
db	2041	ATTAAAAAAGGAAAAA 2059	
db	2495	ATTAAAAAAGGAAAAA 2513	
RESULT 6	AB032975	5814 bp mRNA linear	PRI 17-MAY-2001
LOCUS	Homo sapiens mRNA for KIAA1149 protein, partial cds.		
DEFINITION	AB032975		
ACCESSION	AB032975.2	GI:14133242	
VERSION			
KEYWORDS			
SOURCE			
GANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			

Db 1043 TCTGTAAAGCAGACCCAGTTCCTCCCAAGCTCTCTCCCTGCAGCTTTGTGGTGCCTT 1102
QY 660 CCCCTCAACAGTCTGAAGTCTGGCTCTCTCGGAGGAGCATGATCATTTGGAGGTAT 719
Db 1103 CCCCTCAACAGTCTGAAGTCTGGCTCTCTCGGAGGAGCATGATCATTTGGAGGTAT 1162
QY 720 CGACACTCGTGTACACAGGAGTCTCTGGTATACACCCATCCCGCGGGAGTGTATTA 779
Db 1163 CGACACTCGTGTACACAGGAGTCTCTGGTATACACCCATCCCGCGGGAGTGTATTA 1222
QY 780 TGAGTCAATATTTGGCGGTGGAGATCAATGGACAGGATCTGAATAATGGAGTCAAGGA 839
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QY 840 GTACAACTATGACAAAGACATTTGGACAGTGGCACCAACCACTTCGTTGCCCAAGAA 899
Db 1283 GTACAACTATGACAAAGACATTTGGACAGTGGCACCAACCACTTCGTTGCCCAAGAA 1342
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QY 1140 TTACAAGTTTGGCATCTCACAGTCAATCCAGGGCACTGTATGGAGCTGTATCATGGA 1199
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QY 1260 CATGTGCAGATGATTTGAGGAGCGGAGCGGTGGAGCGCCTTTGTACCTTGGACAT 1319
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QY 1320 GGAAGACTGTGGCTACACATTCACACAGATGATGATCAACCTCATGACCATAGCCTA 1379
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QY 1380 TGTCTATGGCTGCGCTCTTCTCATGTGCTCACTCTGCTCATGCTGCTGTGTGTCAGTG 1439
Db 1823 TGTCTATGGCTGCGCTCTTCTCATGTGCTCACTCTGCTCATGCTGCTGTGTGTCAGTG 1882
QY 1440 GCGTGTCCCTGCGCTGCGCCAGCAGCATGATGACTTTGCTGATGATCATCTCCCTGCT 1499
Db 1883 GCGTGTCCCTGCGCTGCGCCAGCAGCATGATGACTTTGCTGATGATCATCTCCCTGCT 1942
QY 1500 GNAATGAGGAGGCCCCATGGGCAAGATAGAGATTTCCCTTGACACACACTCCCTGGTTC 1559
Db 1943 GNAATGAGGAGGCCCCATGGGCAAGATAGAGATTTCCCTTGACACACACTCCCTGGTTC 2002
QY 1560 ACTTTGGTCAAGTATGAGAGACACAGATGGCACCTGTGGCCAGACACCTCAGGACCTC 1619
Db 2003 ACTTTGGTCAAGTATGAGAGACACAGATGGCACCTGTGGCCAGACACCTCAGGACCTC 2062
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Db 2063 CCCACCCACCAATGCCTCTGCTGTATGGAGAGAAAGCTGGCAAGTGGGTTCGA 2122
QY 1680 GGGACTGTACCTGTAGGAACAGAAAGAGAAAGCAAGCACTCTGCTGGCGGAATAC 1739

Db 2123 GGGACTGTACCTGTAGGAACAGAAAGAGAAAGCACTCTGCTGGCGGAATAC 2182
QY 1740 TCTTGGTCACTCAAAATTTAAGTCGGAAATTCCTGCTGCTCAAACTTCAGCCCTGAACC 1799
Db 2183 TCTTGGTCACTCAAAATTTAAGTCGGAAATTCCTGCTGCTGAAACTTCAGCCCTGAACC 2242
QY 1800 TTTGTCCACCAATTCCTTTAAATTCCTCAACCCAAAGTATTCCTTTCTTTAGTTTCAGA 1859
Db 2243 TTTGTCCACCAATTCCTTTAAATTCCTCAACCCAAAGTATTCCTTTCTTTAGTTTCAGA 2302
QY 1860 AGTACTGGCATCACAGCAGGTACTTGGCGGTGTGTCCTGTGTGTACCTGGCAGAGAA 1919
Db 2303 AGTACTGGCATCACAGCAGGTACTTGGCGGTGTGTCCTGTGTGTACCTGGCAGAGAA 2362
QY 1920 GAGACCAAGCTTGTTCCTGCTGGCCAAAGTCACTAGGAGAGTGCACAGTTTGCAT 1979
Db 2363 GAGACCAAGCTTGTTCCTGCTGGCCAAAGTCACTAGGAGAGTGCACAGTTTGCAT 2422
QY 1980 TTGCTTTAGAGACAGGACTGTATTAACAAGCTTAACATTTGGTGCACAAAGATTGCCTCTTG 2039
Db 2423 TTGCTTTAGAGACAGGACTGTATTAACAAGCTTAACATTTGGTGCACAAAGATTGCCTCTTG 2482
QY 2040 AATTAAAAAATAAAAAA 2059
Db 2483 AATTAAAAAATAAAAACTAGA 2502

RESULT 7
AR178469
LOCUS AR178469 2541 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6319689.
ACCESSION AR178469
VERSION AR178469.1 GI:20219607
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2541)
AUTHORS Powell,D.J., Chapman,C.G., Murphy,K. and Smith,T.S.
TITLE ASP2
JOURNAL Patent: US 6319689-A 1 20-NOV-2001;
FEATURES Location/Qualifiers
source 1..2541
BASE COUNT 598 a 673 c 675 g 579 t 16 others
ORIGIN
Query Match 98.2%; Score 2032; DB 6; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 1 ATGGCCCAAGCCCTCCCTGGCTCTGCTGGATGGCGGGGAGTGTGCTGCCAC 60
Db 1 ATGGCCCAAGCCCTCCCTGGCTCTGCTGGATGGCGGGGAGTGTGCTGCCAC 60
QY 61 GGCACCCAGCAGCGCATCCGCTGCCCTGTGCAGCGGCTGGGGGGGCGCCCTGGGG 120
Db 61 GGCACCCAGCAGCGCATCCGCTGCCCTGTGCAGCGGCTGGGGGGGCGCCCTGGGG 120
QY 121 CTGGGGTGGCCCCGGGAGACCGACGAAGCCCGAGAGCCCGCGGAGGGGAGCTTT 180
Db 121 CTGGGGTGGCCCCGGGAGACCGACGAAGCCCGAGAGCCCGCGGAGGGGAGCTTT 180
QY 181 GTGGAGATGGTGGACAACTGAGGGGCAAGTCTAGCTGGAGATGACC 240
Db 181 GTGGAGATGGTGGACAACTGAGGGGCAAGTCTAGCTGGAGATGACC 240
QY 241 GTGGAGCCGCCGCCAGACGCTCAACATCTCTGTGGATACAGGAGGAGTAACTTGA 300
Db 241 GTGGAGCCGCCGCCAGACGCTCAACATCTCTGTGGATACAGGAGGAGTAACTTGA 300
QY 301 GTGGGTGTGCCCCCAGCCCTTCTGCTACTACAGGAGGAGCTGTCCAGACA 360

Db	1	ATGCCCAAGCCCTGCCCTGGCTCTGCTGTGATGGCGCGGAGTGTGCTGCTGCCAC	60
Qy	61	GGCACCAGCACGGCATCCGGCTGCCCTTCGCGACAGCGGCTTGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCAGCACGGCATCCGGCTGCCCTTCGCGACAGCGGCTTGGGGGCGCCCCCTGGGG	120
Qy	121	CTCGGGTCCCGGGAGACCGACGAGACCGAGACCGGCGGAGAGCCCGCGGAGGCGAGCTTT	180
Db	121	CTCGGGTCCCGGGAGACCGACGAGACCGGAGACCGGCGGAGAGCCCGCGGAGGCGAGCTTT	180
Qy	181	GTGGAGATGTTGACAACTGAGGGCACTGCGGGCAGTGTGCGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGTTGACAACTGAGGGCACTGCGGGCAGTGTGCGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGAGCCCCCGGACAGCGCTCAACATCCTCGTGGATACAGGACGACGTAACCTTTGCA	300
Db	241	GTGGGAGCCCCCGGACAGCGCTCAACATCCTCGTGGATACAGGACGACGTAACCTTTGCA	300
Qy	301	GTGGTGTCTGCCCCCCCAGCCCTTCTCTGTCATCGTCTACTACAGAGGACGTGTCCAGCAC	360
Db	301	GTGGTGTCTGCCCCCCCAGCCCTTCTCTGTCATCGTCTACTACAGAGGACGTGTCCAGCAC	360
Qy	361	TACCGGACCTCGGAGGTTGTATGTGCCCTACACCAGGCGAAGTGGGAAGGGGAG	420
Db	361	TACCGGACCTCGGAGGTTGTATGTGCCCTACACCAGGCGAAGTGGGAAGGGGAG	420
Qy	421	CTGGGACCCGACCTGTTAAGCATCCCCATCGGCCCAACGCTCACTGTGCGTGCACACATT	480
Db	421	CTGGGACCCGACCTGTTAAGCATCCCCATCGGCCCAACGCTCACTGTGCGTGCACACATT	480
Qy	481	GCTGCCATCTACTGAATCAGACAAAGTTCTTCAACGGCTCCAACTGGGAAGCATCCTTG	540
Db	481	GCTGCCATCTACTGAATCAGACAAAGTTCTTCAACGGCTCCAACTGGGAAGCATCCTTG	540
Qy	541	GGGCTGCCCTTACTCTGAGATTGCCAGGCTTGACGACTCCCTGAGCCCTTCTTTGACTCT	600
Db	541	GGGCTGCCCTTACTCTGAGATTGCCAGGCTTGACGACTCCCTGAGCCCTTCTTTGACTCT	600
Qy	601	CTGTTAAGCAGACCCACGTTCCCACTCTTCTCCTGCACCTTTGTGTGCTGGCTTC	660
Db	601	CTGTTAAGCAGACCCACGTTCCCACTCTTCTCCTGCACCTTTGTGTGCTGGCTTC	660
Qy	661	CCCTCAACAGTCTGAAGTCTGGGCTCTGTGCGAGGAGCATGATCATTTGAGGTATC	720
Db	661	CCCTCAACAGTCTGAAGTCTGGGCTCTGTGCGAGGAGCATGATCATTTGAGGTATC	720
Qy	721	GACCACTCGTGTACACAGGACGCTCTGTGTATACACCAATCCGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGTGTACACAGGACGCTCTGTGTATACACCAATCCGCGGGAGTGGTATTAT	780
Qy	781	GAGGTATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTCAAGGAG	840
Db	781	GAGGTATCATTTGTGGGGTGGAGATCAATGGACAGGATCTGAAATGGACTCAAGGAG	840
Qy	841	TACAACCTATGACAGAGCATTTGGACAGTGGCACCCACCAACCTTCGTTTGCCTCAAGAAA	900
Db	841	TACAACCTATGACAGAGCATTTGGACAGTGGCACCCACCAACCTTCGTTTGCCTCAAGAAA	900
Qy	901	GTGTTTGAAGCTGGAGTCAATCCATCAAGGACGCTCTCTCCAGGAGAAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGGAGTCAATCCATCAAGGACGCTCTCTCCAGGAGAAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTTAGGAGACGCTGGTGTCTGCGAAGCAGGACCCCTTGGACACATT	1020
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Qy	1021	TTCCAGTCTACTCTACTTAATGGGTGAGGTTACCAACCAAGTCTTCCGATCACC	1080
Db	1021	TTCCAGTCTACTCTACTTAATGGGTGAGGTTACCAACCAAGTCTTCCGATCACC	1080
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RESULT 9	
E50816	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	

KEYWORDS	JP 2000060579-A/1.
SOURCE	unidentified.
ORGANISM	unidentified
REFERENCE	1 (bases 1 to 2541)
AUTHORS	David,J.P., Conrad,G.C., Kay,M. and Trudy,S.S.
TITLE	Aspartate proteinase ASP2
JOURNAL	Patent: JP 2000060579-A 1 29-FEB-2000;
COMMENT	SMITHKLINE BEECHAM CORP OS Unidentified PN JP 2000060579-A/1 PD 29-FEB-2000 PF 03-AUG-1999 JP 1999219665 PR 28-JAN-1997 GB 9701684.4 PI DAVID J POWERU,CONRAD G CHAPPUMAN,KAY WAFI,TRUDY S SMITH PC C12N15/09,A61K31/7088,A61K38/46,A61K39/00,A61K39/395,PC A61K39/395,A61K48/00, PC A61P25/28,A61P35/00,A61P43/00,C07K16/40,C12N1/15,C12N1/19,PC C12N1/21, PC C12N5/10,C12N9/64,C12Q1/37,G01N33/15,G01N33/50,G01N33/53,PC G01N33/566, PC G01N33/577/C12P21/08,C12N15/00,A61K37/54,C12N5/00 CC Strandedness: Single; CC Topology: Linear; FH Key: Location/Qualifiers FT source 1..2541 FT /organism='Unidentified'. FEATURES source Location/Qualifiers 1..2541 /organism='unidentified' /db_xref='taxon:32644' BASE COUNT 598 a 673 c 579 t 16 others ORIGIN Query Match 98.2%; Score 2032; DB 6; Length 2541; Best Local Similarity 99.5%; Pred. No. 0; Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1; QY 1 ATGGCCCAAGGCCCTGCCTTCTGTGGATGGCGGGGAGTGCTGCTGCCAC 60 DB 1 ATGGCCCAAGGCCCTGCCTTCTGTGGATGGCGGGGAGTGCTGCTGCCAC 60 QY 61 GGCACCCAGCAGCATCCGCTGCCCTGGCAGCGCCTGGGGGCGCCCCCTGGG 120 DB 61 GGCACCCAGCAGCATCCGCTGCCCTGGCAGCGCCTGGGGGCGCCCCCTGGG 120 QY 121 CTGCGGCTGCCCGGGAGACCGAGAGAGCCGAGGAGCCGCGCGGAGGGCAGCTTT 180 DB 121 CTGCGGCTGCCCGGGAGACCGAGAGAGCCGAGGAGCCGCGCGGAGGGCAGCTTT 180 QY 181 GTGGAGATGGTGGACAACCTGAGGGGGAAGTCGGGGCAGGCTACTAGTGGAGATGACC 240 DB 181 GTGGAGATGGTGGACAACCTGAGGGGGAAGTCGGGGCAGGCTACTAGTGGAGATGACC 240 QY 241 GTGGCAGCCCCCGCACAGCCTCAACATCTGTGTGGATACAGGCAGCAGTAACCTTGA 300 DB - 241 GTGGCAGCCCCCGCACAGCCTCAACATCTGTGTGGATACAGGCAGCAGTAACCTTGA 300 QY 301 GTGGGTGTGCCCCCCCACCCCTTCCTGATCGCTACTACAGAGCAGCTGTCCAGCACA 360 DB 301 GTGGGTGTGCCCCCCCACCCCTTCCTGATCGCTACTACAGAGCAGCTGTCCAGCACA 360 QY 361 TACCGGGACCTCCGGAAGGCTGTGTATGTCCTACACCCAGGGCAAGTGGGAAGGGGAG 420 DB 361 TACCGGGACCTCCGGAAGGCTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420 QY 421 CTGGGCACCGACCTGTGTAAAGTATCCCCATGCCCCCAACGTCATGTGCGTGCCAACATT 480 DB 421 CTGGGCACCGACCTGTGTAAAGTATCCCCATGCCCCCAACGTCATGTGCGTGCCAACATT 480 QY 481 GTGTGCATCACTGAATCAGACAAGTTCTTTCATCAGCGCTCCAACCTGGGAAGGCATCCTG 540 DB 481 GTGTGCATCACTGAATCAGACAAGTTCTTTCATCAGCGCTCCAACCTGGGAAGGCATCCTG 540

Db 961 GGCACCCCTTGGACATTTTCCAGTCACTACCTACCTAAATGGGTGAGTTACC 1020
Qy 1060 AACAGTCTCTCCGATCACCATCTTCCGAGCAATACCTGCGGCAGTGAAGATGTG 1119
Db 1021 AACAGTCTCTCCGATCACCATCTTCCGAGCAATACCTGCGGCAGTGAAGATGTG 1080
Qy 1120 GCCAGTCCCAAGACGACTGTTACAGTTTCCCATCTCACAGTCAATCCACGGGCACTGTT 1179
Db 1081 GCCAGTCCCAAGACGACTGTTACAGTTTCCCATCTCACAGTCAATCCACGGGCACTGTT 1140
Qy 1180 ATGGAGCTGTATCATGGAGGCTTCTACCTTGTCTTGTGATCGGCGCCGAAACGAAAT 1239
Db 1141 ATGGAGCTGTATCATGGAGGCTTCTACCTTGTCTTGTGATCGGCGCCGAAACGAAAT 1200
Qy 1240 GGCTTTGCTGACGCGCTTGCCATGTGACAGTATGAGTTTCAGGAGCGGCGGTGGAAGC 1299
Db 1201 GGCTTTGCTGACGCGCTTGCCATGTGACAGTATGAGTTTCAGGAGCGGCGGTGGAAGC 1260
Qy 1300 CCTTTGTCACCTTGGACATGGAGACTGTGGCTACACATTCACAGACAGATGAGTCA 1359
Db 1261 CCTTTGTCACCTTGGACATGGAGACTGTGGCTACACATTCACAGACAGATGAGTCA 1320
Qy 1360 ACCCTCATGACATAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1419
Db 1321 ACCCTCATGACATAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Qy 1420 TGCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1479
Db 1381 TGCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Qy 1480 GCTGATGACATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1539
Db 1441 GCTGATGACATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Qy 1540 GGACACACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1599
Db 1501 GGACACACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Qy 1600 CAGAGCACCCTCAGGACCCCTCCACCCACCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
Db 1561 CAGAGCACCCTCAGGACCCCTCCACCCACCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Qy 1660 GCCTGGCAGTGGGTTCCAGGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAAAG 1719
Db 1621 GCCTGGCAGTGGGTTCCAGGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAAAG 1680
Qy 1720 CACTCTGCTGCGGGAATACCTTGTGCTACCTCAAAATTTAAGTCGGGAAATTTCTGCTGCT 1779
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Qy 1780 TGAACCTTCAGCCCTGAACTTTGTCCACCATTCCTTTAAATTTCTCAACCCCAAGTATT 1839
Db 1741 TGAACCTTCAGCCCTGAACTTTGTCCACCATTCCTTTAAATTTCTCAACCCCAAGTATT 1800
Qy 1840 CTTCTTTCTTAGTTTTCAGAGTACTTGGCATCACACGAGGTTTACCTTGGCGGTGTGCTCC 1899
Db 1801 CTTCTTTCTTAGTTTTCAGAGTACTTGGCATCACACGAGGTTTACCTTGGCGGTGTGCTCC 1860
Qy 1900 TGTGTTACCTTGGCAGAGACAGACAGCTTGTTCCTGCTGCGCCAAAGTCAGTAGGA 1959
Db 1861 TGTGTTACCTTGGCAGAGAGACAGACAGCTTGTTCCTGCTGCGCCAAAGTCAGTAGGA 1920
Qy 1960 GAGGATGCACAGTTTGTCTTATTTGCTTTAGACAGAGGACTGTATAAACAGCCTAACATT 2019
Db 1921 GAGGATGCACAGTTTGTCTTATTTGCTTTAGACAGAGGACTGTATAAACAGCCTAACATT 1980
Qy 2020 GGTGAAAGATTGCTCTTGAATTTAAATAAAAAA 2057
Db 1981 GGTGAAAGATTGCTCTTGAATTTAAATAAAAAA 2018

RESULT 12
AX472368

LOCUS AX472368 3252 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1 from Patent WO02053594.
ACCESSION AX472368
VERSION AX472368.1 GI:22207364
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Ghosh,A.K., Koelsch,G. and Tang,J.J.
TITLE Inhibitors of menapsin 2 and use thereof
JOURNAL Patent: WO 02053594-A 1 11-JUL-2002;
OKLAHOMA MED RES FOUND (US); TRUSTEES OF THE UNIVERSITY OF ILLINOIS
(US)
FEATURES
source Location/Qualifiers
1..3252
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 804 a 863 c 811 g 771 t 3 others
ORIGIN
Query Match 97.1%; Score 2010; DB 6; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 40 GCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 99
Db 1 GCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy 100 CTGGGGGCGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 159
Db 61 CTGGGGGCGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 160 CCCGCCGAGGCGGCGAGCTTTGTGAGATGTGTGACACCTTGAGGGGGAAGTCGGGGGAG 219
Db 121 CCCGCCGAGGCGGCGAGCTTTGTGAGATGTGTGACACCTTGAGGGGGAAGTCGGGGGAG 180
Qy 220 GCCTACTACGTGGAGATGACCTGGGAGCCCGGCGAGAGCTCAACATCTGCTGCTGCTGCT 279
Db 181 GCCTACTACGTGGAGATGACCTGGGAGCCCGGCGAGAGCTCAACATCTGCTGCTGCTGCT 240
Qy 280 ACAGGACAGTAACTTTGCAGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 339
Db 241 ACAGGACAGTAACTTTGCAGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 340 CAGAGGCGAGCTGTCCAGCACATACCGGACCTCCCGAAGGCTGTGTATGTCCTTACACC 399
Db 301 CAGAGGCGAGCTGTCCAGCACATACCGGACCTCCCGAAGGCTGTGTATGTCCTTACACC 360
Qy 400 CAGGCAAGTGGGAAGGAGCTGGGACACCGACCTGTTAAGCATCCCGCATGGGCGCCCAAC 459
Db 361 CAGGCAAGTGGGAAGGAGCTGGGACACCGACCTGTTAAGCATCCCGCATGGGCGCCCAAC 420
Qy 460 GTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
Db 421 GTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 520 TCCAACTGGGAAGGAGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 579
Db 481 TCCAACTGGGAAGGAGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 580 CTGGAGCCTTTCTTTGACTCTCTGTAAGCAGACCCACCTTCCCAACCTCTCTCTCCCTG 639
Db 541 CTGGAGCCTTTCTTTGACTCTCTGTAAGCAGACCCACCTTCCCAACCTCTCTCTCCCTG 600
Qy 640 CACCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
Db 601 CAGCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy 700 AGCATGATCATTTGGAGGTATCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db 661 AGCATGATCATTTGGAGGTATCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

Qy	100	CTGGGGGGCGCCCTTGGGGCTGGCGCTGGCCGGGAGACCGACGAAGAGCCCGGAGGAG	159
Db	61	CTGGGGGGCGCCCTTGGGGCTGGCGCTGGCCGGGAGACCGACGAAGAGCCCGGAGGAG	120
Qy	160	CCGGCCGGAGGGCAGCTTTGTGGAGATGGTGACAACTGAGGGGCAAGTCGGGGCAG	219
Db	121	CCGGCCGGAGGGCAGCTTTGTGGAGATGGTGACAACTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCGCCACCCCTTCCTGCGATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCGCCACCCCTTCCTGCGATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGAGCTCCGGAAAGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGAGCTCCGGAAAGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTTGTAAAGCATCCCGCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTTGTAAAGCATCCCGCATGGCCCCAAC	420
Qy	460	GTCACTCTGGTGCCCAACATGTCTGCCATCAGTCAGTAATCAGACAGTTCTTCATCAACGGC	519
Db	421	GTCACTCTGGTGCCCAACATGTCTGCCATCAGTCAGTAATCAGACAGTTCTTCATCAACGGC	480
Qy	520	TCCAACGTGGAAGGCATCCTGGGGCTGGCCCTATGCTCAGATGTGCAGGCGCTGACGACTCC	579
Db	481	TCCAACGTGGAAGGCATCCTGGGGCTGGCCCTATGCTCAGATGTGCAGGCGCTGACGACTCC	540
Qy	580	CTGSAGCCTTCTTTGACTCTCTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGSAGCCTTCTTTGACTCTCTGGTAAAGCAGACCCACGCTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGTGCTTCCCGCTCAACAGTCTGAAGTGTGTGGCTCTGTGCGAGGG	699
Db	601	CAGCTTTGTGGTGTGCTTCCCGCTCAACAGTCTGAAGTGTGTGGCTCTGTGCGAGGG	660
Qy	700	AGCATGATCATTTGGAGGTATCGACACTTCGCTGTACACAGCGAGTCTCTGGTATACACC	759
Db	661	AGCATGATCATTTGGAGGTATCGACACTTCGCTGTACACAGCGAGTCTCTGGTATACACC	720
Qy	760	ATCCGGCGGAGTGGTATTATGAGGTGCATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGAGTGGTATTATGAGGTGCATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAATGACATGCAAGGAGTACAACTATGACAAAGAGCATTTGFGAGAGTGGCACCAACC	879
Db	781	CTGAAATGACATGCAAGGAGTACAACTATGACAAAGAGCATTTGFGAGAGTGGCACCAACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTGGAAGCTGCAGTCAAACTCAAGGAGAGCCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTGGAAGCTGCAGTCAAACTCAAGGAGAGCCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACACCCCTTGGGAACATTTTCCAGTGCATCTCACTTAATGGGTGAGGTTACC	1059
Db	961	GGCACACCCCTTGGGAACATTTTCCAGTGCATCTCACTTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAAGTCTTCGCGATCACCTCTCCGACCAATACCTGGCGCCAGTGGAGATGTG	1119
Db	1021	AACCAAGTCTTCGCGATCACCTCTTCGCGACCAATACCTGGCGCCAGTGGAGATGTG	1080
Qy	1120	GCCAGTCCCAAGACGACTGTTACAAGTTTGGCATCTCACAGTCATCCACGGGCAGTGTT	1179
Db	1081	GCCAGTCCCAAGACGACTGTTACAAGTTTGGCATCTCACAGTCATCCACGGGCAGTGTT	1140
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[illegible]

TITLE Novel nucleic acid and amino acid sequences		901		GTGTTTGAAGCTGACGCTCAATCCATCAAGCAGGCTCTCCACGAGAGTTCCTGAT	960
JOURNAL Patent: WO 0206315-A 84 24-JAN-2002;		1280		GGTTTGAAGCTGACGCTCAATCCATCAAGCAGGCTCTCCACGAGAGTTCCTGAT	1339
CompuGen Ltd. (IL)					
FEATURES Location/Qualifiers		961		GGTTTCTGGCTAGGAGAGCAGCTGTGCTGGCAAGCAGGACACCCCTTGGACATTT	1020
source 1..5757		1340		GGTTTCTGGCTAGGAGAGCAGCTGTGCTGGCAAGCAGGACACCCCTTGGACATTT	1399
BASE COUNT 1485 a 1490 c 1392 g 1388 t 2 others		1021		TTCCCAAGTCTACCTACTCTACCTAATGGGTGAGGTACCAACAGTTCCTCCGATCACC	1080
ORIGIN		1400		TTCCCAAGTCTACCTACTCTACCTAATGGGTGAGGTACCAACAGTTCCTCCGATCACC	1459
Query Match 91.5%; Score 1894.2; DB 6; Length 5757;		1081		ATCCTTCCCGCAGCAATACCTGGCGCAGTGGGAAGATGTGGCCACAGTCCCAAGACGACTGT	1140
Best Local Similarity 96.2%; Pred. No. 0;		1460		ATCCTTCCCGCAGCAATACCTGGCGCAGTGGGAAGATGTGGCCACAGTCCCAAGACGACTGT	1519
Matches 1981; Conservative 0; Mismatches 3; Indels 75; Gaps 1;		1141		TACAAGTTTGGCCATCTCAGAGTATCCAGGGGACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy 1 ATGGCCCAAGCCCTGGCCCTGGCTCTGCTGTGATGGGCGCGGAGTGTGCTGCCAC		1520		TACAAGTTTGGCCATCTCAGAGTATCCAGGGGACTGTTATGGGAGCTGTTATCATGGAG	1579
Db 455 ATGGCCCAAGCCCTGGCCCTGGCTCTGCTGTGATGGGCGCGGAGTGTGCTGCCAC		1201		GGCTTCTACGTTGTCTTTGATCGGGCCGAAACAGAAATGGCTTTCCTGTCAGCGCTTGC	1260
Qy 61 GGCACCCAGCAGCGCATCCGGCTGCCCTTGGCAGCGGCTGGGGGCGGCCCTCGGGG		1580		GGCTTCTACGTTGTCTTTGATCGGGCCGAAACAGAAATGGCTTTCCTGTCAGCGCTTGC	1639
Db 515 GGCACCCAGCAGCGCATCCGGCTGCCCTTGGCAGCGGCTGGGGGCGGCCCTCGGG		1261		CATGTGCACGATGAGTTTCAAGGCGGCGGTGGAAAGGCCCTTTTGTCACTTTGGACATG	1320
Qy 121 CTGGGCTGCCCGGAGACGACGAGAGGCCGAGGAGCCCGGCGGAGGGGAGGCTTT		1640		CATGTGCACGATGAGTTTCAAGGCGGCGGTGGAAAGGCCCTTTTGTCACTTTGGACATG	1699
Db 575 CTGGGCTGCCCGGAGACGACGAGAGGCCGAGGAGCCCGGCGGAGGGGAGGCTTT		1321		GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1380
Qy 181 GTGGAGATGTGGAACTTGGAGGCAAGTGGGGGAGGCTTACTAGTGGAGATGACC		1700		GAAGACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1759
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Db 815 TACCGGACCTCCCGAAGGTTGTATGTGCTTACACCCAGGCAAGTGGGAGGGAG		1561		CTTTGTGTACAAGTAGAGACACAGATGGACCTGTGGCCAGAGACCTCAGACCCCTCC	1620
Qy 421 CTGGGACCGACCTGTTAAGCATCCCGATGGGCCCAAGTCACTGTGCTGCCAATTT		1940		CTTTGTGTACAAGTAGAGACACAGATGGACCTGTGGCCAGAGACCTCAGACCCCTCC	1999
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Qy 481 GCTGCCATCACTGAATCAGCAAGTCTTTCATCAACGCTCCCACTGGGAAGGCACTCG		2000		CCACCCACCAATGCTCTGCTCTGCTGATGGAGAGGAAAGGCTGGCAAGGTGGTTCAG	2059
Db 935 GCTGCCATCACTGAATCAGCAAGTCTTTCATCAACGCTCCCACTGGGAAGGCACTCG		1681		GGACTGTACCTGTAGGAACACAGAAAGAGAAAGACACTCTGCTGCGGGGAATACT	1740
Qy 541 GGGCTGGCTTATGCTGATTTGCCAGGCTGACGACTCCCTGGAGCCCTTTCTTTGACTCT		2060		GGACTGTACCTGTAGGAACACAGAAAGAGAAAGAGACACTCTGCTGCGGGGAATACT	2119
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Db 1022 -----		1801		TTGTCCACCAATTCCTTTAAATTTCCCAACCCCAAGATTTCTCTTTTCTTTAGTTTCAGAA	1860
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Db 1040 CCCCTCAACAGTCTGAAGTCTGGCCCTCTGCGAGGAGCATGATCATTTGGAGGTATC		1861		GTACTGGCATCACAGCAGGTTACCTTTGGGCTGTGCTCCCTGTGCTGCTGCTGGCAGAG	1920
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QY 1991 TGCTTTAGACACAGGACTGTATTAACAAGCCTAACATTTGTCGAAAGATTGCCTCTTTGA 2040
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Db 2360 TGCTTTAGACACAGGACTGTATTAACAAGCCTAACATTTGTCGAAAGATTGCCTCTTTGA 2419
QY 2041 ATTAATAAAAAAAAAAAAAA 2059
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Db 2420 ATTAATAAAAAAAAAAACTAGA 2438
RESULT 15
AX105387
LOCUS AX105387 1977 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0123533.
ACCESSION AX105387
VERSION AX105387.1 GI:13921512
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1977)
AUTHORS Gurney,M. and Bienkowski,M.J.
TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor
JOURNAL Patent: WO 0123533-A 5 05-APR-2001;
Pharmacia & Upjohn Company (US)
FEATURES Location/Qualifiers
source 1..1977
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/db_xref="taxon:9606"
BASE COUNT 447 a 552 c 551 g 427 t
ORIGIN
Query Match 91.2%; Score 1887.2; DB 6; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;
QY 1 ATGCCCCAAGCCCTGCCCTGCTCTGCTGTGGATGGCGCGGAGTGCTGCCCTGCCAC 60
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QY 121 CTGCGGCTGCCCGGGAGACCGACGAGAGCCGAGGAGCCGCCGCGGAGGCGAGCTTT 180
Db 121 CTGCGGCTGCCCGGGAGACCGACGAGAGCCGAGGAGCCGCCGCGGAGGCGAGCTTT 180
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181 GTGGAGATGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTAGTGGAGATGACC 240
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QY 301 GTGGGTGTGCCCCCCCCCTTCTGTCATCGCTACTACAGAGGCGAGCTGTCCAGCACA 360
Db 301 GTGGGTGTGCCCCCCCCCTTCTGTCATCGCTACTACAGAGGCGAGCTGTCCAGCACA 360
QY 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTTACACCCAGGCGAAGTGGGAAGGGGAG 420
Db 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTTACACCCAGGCGAAGTGGGAAGGGGAG 420
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Db 421 CTGGGACCGACCTCGGTAAAGCATCCCGCATGGCCCGCAACGCTACTGTGCGTGCACAATT 480
QY 481 GCTGCATCTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGATCCTG 540
Db 481 GCTGCATCTGAATCAGACAAAGTTCTTTCATCAACGGCTCCAACTGGGAAGGATCCTG 540

QY 541 GGGCTGGCCTATGTCTGAGATTGCCAGGCTTCCAGACTCCCTGGAGCCTTTCTTTTACTCT 600
|||||
Db 541 GGGCTGGCCTATGTCTGAGATTGCCAGG-----
QY 601 CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGACACCTTTGTGGTGGCTGGCTTC 660
|||||
Db 568 -----CTTTGTGGTGGCTGGCTTC 585
QY 661 CCCCTCAACCAAGTCTGAAGTCTGCTGGCCTCTCTCGGAGGGAGCATGATCATTTGGAGGTATC 720
|||||
Db 586 CCCCTCAACCAAGTCTGAAGTCTGCTGGCCTCTCTCGGAGGGAGCATGATCATTTGGAGGTATC 645
QY 721 GACCACCTGCTGTATACACAGGAGTCTCTGTGTATACACCCATCCCGCGGAGTGGTATTAT 780
|||||
Db 646 GACCACCTGCTGTATACACAGGAGTCTCTGTGTATACACCCATCCCGCGGAGTGGTATTAT 705
QY 781 GAGTCTATCATTTGCGGGTGGAGATCAATCGACAGGATCTGAAAATGGAGCTGCAAGAG 840
|||||
Db 706 GAGTGTGATCATTTGTGCGGGTGGAGATCAATCGACAGGATCTGAAAATGGAGCTGCAAGAG 765
QY 841 TACAACCTATGACAAAGCATTGTGGACAGTGGCACACCAACCTTCTGTTTCCCAAGAAA 900
|||||
Db 766 TACAACCTATGACAAAGCATTGTGGACAGTGGCACACCAACCTTCTGTTTCCCAAGAAA 825
QY 901 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGCAGCCTCTCCACGGAGAAAGTTCCCTGAT 960
|||||
Db 826 GTGTTTGAAGCTGCAGTCAAAATCCATCAAGCAGCCTCTCCACGGAGAAAGTTCCCTGAT 885
QY 961 GGTGTTGGCTAGGAGAGCAGCTGGTGTGGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1020
Db 886 GGTGTTGGCTAGGAGAGCAGCTGGTGTGGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 945
QY 1021 TTCCAGTCTACCTTACCTTAATGGTGGAGTGTACCAACCAAGTCTTCCCGATCACC 1080
Db 946 TTCCAGTCTACCTTACCTTAATGGTGGAGTGTACCAACCAAGTCTTCCCGATCACC 1005
QY 1081 ATCCTTCCGACGAATACCTCGGCCAGTGGGAAGATGTGGCAGCTCCCAAGAGAGCTGT 1140
Db 1006 ATCCTTCCGACGAATACCTCGGCCAGTGGGAAGATGTGGCAGCTCCCAAGAGAGCTGT 1065
QY 1141 TACAAGTTTGGCATCTCACAGTCTCACAGGGGCACTGTTATGGAGCTGTTATCATGGAG 1200
Db 1066 TACAAGTTTGGCATCTCACAGTCTCACAGGGGCACTGTTATGGAGCTGTTATCATGGAG 1125
QY 1201 GCCTTCTACGTTGCTTTGATCGGGCCGAAAAGCAATTTGGCTTGTCTCAGCGCTTGC 1260
Db 1126 GCCTTCTACGTTGCTTTGATCGGGCCGAAAAGCAATTTGGCTTGTCTCAGCGCTTGC 1185
QY 1261 CATGTGCACGATGATTTTCAGGACGGCAGCGGTGGAAAGGCCCTTTTGTACACCTTGGACATG 1320
Db 1186 CATGTGCACGATGATTTTCAGGACGGCAGCGGTGGAAAGGCCCTTTTGTACACCTTGGACATG 1245
QY 1321 GAAACACTGTGGCTACACATTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGACCTAT 1380
Db 1246 GAAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCCCTCATGACCATAGACCTAT 1305
QY 1381 GTCATGGCTGCACTCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGTTGTGTGTCAGTGG 1440
Db 1306 GTCATGGCTGCACTCTGCGCCCTCTTCATGCTGCCACTCTGCCCTCATGTTGTGTGTCAGTGG 1365
QY 1441 CGTGTCCCTCCCTGCCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Db 1366 CGTGTCCCTCCCTGCCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1425
QY 1501 AAGTGAAGGAGGCCCATGGGCAAGAGATAGAGATTTCCCTTGGACACACACCTCCGCTGGTTCA 1560
Db 1426 AAGTGAAGGAGGCCCATGGGCAAGAGATAGAGATTTCCCTTGGACACACACCTCCGCTGGTTCA 1485
QY 1561 CTTTGGTTCACAAGTGAAGGACACAGATGGGCACTGTGGCCAGAGACCTCAGGAGCCCTCC 1620
Db 1486 CTTTGGTTCACAAGTGAAGGACACAGATGGGCACTGTGGCCAGAGACCTCAGGAGCCCTCC 1545
QY 1621 CCACCCACCAATGCCTCTGCCTTGTATGGAGAAGAAAAGGCTGGCAAGGTGGTTCAG 1680

[illegible]

Search completed: July 9, 2003, 14:10:34
Job time : 5398 secs

Result No.	Query %	Score	Match	Length	DB	ID	Description
1	2070	100.0	2070	21	AAA15662		Human aspartyl pro
2	2070	100.0	2070	22	AAI17865		Human aspartyl pro
3	2070	100.0	2070	22	AAI13021		Human aspartyl pro
4	2070	100.0	2070	22	AAI11517		Human aspartyl pro
5	2070	100.0	2070	22	AAI11702		Human cDNA encoding
6	2070	100.0	2070	22	AAI06739		Human aspartyl pro
7	2070	100.0	2070	22	ABL52457		Human Asp-2(a) nuc
8	2070	100.0	2070	24	ABL49914		Human aspartyl pro
9	2047.8	98.9	16080	21	AAA59553		DNA clone pCEK C1.

the beta secretase site to produce amyloid beta peptide

Claim 5; Fig 2; 183pp; English.

This sequence represents the human aspartyl protease 2 (Asp2) nucleotide sequence. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence PNG and a sequence encoding DSG or DTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.

Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 21; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCGCCCAAGCCCTGCGCTGGCTCTGCTGGTGGGCGCGGAGTGTGCTGCCAC	60
DB	1	ATGCGCCCAAGCCCTGCGCTGGCTCTGCTGGTGGGCGCGGAGTGTGCTGCCAC	60
QY	61	GGCACCAGCAGCGCATCGGCTGCGCTCGCAGCGGCTGGGGCGCCGCCCTGGGG	120
DB	61	GGCACCAGCAGCGCATCGGCTGCGCTCGCAGCGGCTGGGGCGCCGCCCTGGGG	120
QY	121	CTCGCGTGCCTCGGGAGACCGAGCAAGACCGCGAGAGCCCGCGCGGAGGGCAGCTTT	180
DB	121	CTCGCGTGCCTCGGGAGACCGAGCAAGACCGCGAGAGCCCGCGCGGAGGGCAGCTTT	180
QY	181	GTGGAGATGTGGACAACTGAGGGCAAGTGGGGCAAGTGTACCTGGAGATGACC	240
DB	181	GTGGAGATGTGGACAACTGAGGGCAAGTGGGGCAAGTGTACCTGGAGATGACC	240
QY	241	GTGGGAGCCCCCGGAGAGCGTCAACATCTCTGGTGGATACAGGACAGTAACTTTGCA	300
DB	241	GTGGGAGCCCCCGGAGAGCGTCAACATCTCTGGTGGATACAGGACAGTAACTTTGCA	300
QY	301	GTGGGTGCTGCCGCCACCCCTTCCTGCTGCTACTACAGAGGAGCTGTCCAGCACA	360
DB	301	GTGGGTGCTGCCGCCACCCCTTCCTGCTGCTACTACAGAGGAGCTGTCCAGCACA	360
QY	361	TACCGGACCTCGGAAGGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	420
DB	361	TACCGGACCTCGGAAGGTGTATGTGCCCTACACCCAGGCAAGTGGGAAGGGAG	420
QY	421	CTGGGACCGACCTGGTAAAGCATCCCCCATGGCCCCCAACGTCACTGTGGGTGCCAAT	480
DB	421	CTGGGACCGACCTGGTAAAGCATCCCCCATGGCCCCCAACGTCACTGTGGGTGCCAAT	480
QY	481	GCTGCCATCACTGAATCAGACAAAGTTCTTATCAAGCGCTCCCACTGGGAAGGCATCTG	540
DB	481	GCTGCCATCACTGAATCAGACAAAGTTCTTATCAAGCGCTCCCACTGGGAAGGCATCTG	540
QY	541	GGGCTGGCTTATGCTGAGATGGCAGGCTTGAGGACTCCCTGGAGCTTTCTTTGACTCT	600
DB	541	GGGCTGGCTTATGCTGAGATGGCAGGCTTGAGGACTCCCTGGAGCTTTCTTTGACTCT	600
QY	601	CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCAACCTTTGTGTGCTGCTTC	660
DB	601	CTGGTAAAGCAGACCCAGCTTCCCAACCTCTTCTCCCTGCAACCTTTGTGTGCTGCTTC	660
QY	661	CCCCTCAACAGTCTGAAGTGTGGCTGTGCGGAGGAGCATGATCATTTGAGGTATC	720
DB	661	CCCCTCAACAGTCTGAAGTGTGGCTGTGCGGAGGAGCATGATCATTTGAGGTATC	720

DB	661	CCCCTCAACAGTCTGAAGTGTGGCTGTGCGGAGGAGCATGATCATTTGAGGTATC	720
QY	721	GACCACTCGCTGTACACAGGAGTCTCTGGTATACACCCATCGGGGGAGTGTATTAT	780
DB	721	GACCACTCGCTGTACACAGGAGTCTCTGGTATACACCCATCGGGGGAGTGTATTAT	780
QY	781	GAGTCTCATTTGTCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840
DB	781	GAGTCTCATTTGTCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840
QY	841	TACAACATGACAGAGCATTTGTGAGAGTGGCAGGACCAACCTTCCTTGGCCCAAGAA	900
DB	841	TACAACATGACAGAGCATTTGTGAGAGTGGCAGGACCAACCTTCCTTGGCCCAAGAA	900
QY	901	GTGTTGAAGCTGCAGTCAAAATCCATCAAGCAGCCTCTCCACGGAGAGTTCCTCGAT	960
DB	901	GTGTTGAAGCTGCAGTCAAAATCCATCAAGCAGCCTCTCCACGGAGAGTTCCTCGAT	960
QY	961	GGTTTCTGGCTAGGAGAGCAGTGTGCTGGCAAGCAGCAGCCCTTGGAAACAT	1020
DB	961	GGTTTCTGGCTAGGAGAGCAGTGTGCTGGCAAGCAGCAGCCCTTGGAAACAT	1020
QY	1021	TTCCAGTCATCTCACTCTACCTAATGGTGGTGGTGTACCAACCACTCTTCCGATCACC	1080
DB	1021	TTCCAGTCATCTCACTCTACCTAATGGTGGTGGTGTACCAACCACTCTTCCGATCACC	1080
QY	1081	ATCCTTCCGAGCAATACCTCGGCGCAGTGGAAAGATGTGGCCACGTCCCAAGAGACTGT	1140
DB	1081	ATCCTTCCGAGCAATACCTCGGCGCAGTGGAAAGATGTGGCCACGTCCCAAGAGACTGT	1140
QY	1141	TACAAGTTTGGCATCTCAGTATCCACGGGCTGTATATGGAGCTGTATCATGGAG	1200
DB	1141	TACAAGTTTGGCATCTCAGTATCCACGGGCTGTATATGGAGCTGTATCATGGAG	1200
QY	1201	GGCTTCTACGTGTCTTTGATCGGGCCGCAAAAGAAATGGCTTTGCTGTGAGGCTTGC	1260
DB	1201	GGCTTCTACGTGTCTTTGATCGGGCCGCAAAAGAAATGGCTTTGCTGTGAGGCTTGC	1260
QY	1261	CATGTGCAGTGTGAGTTCAGGACGCGGTGGAAAGCCCTTTTGTGCTTGGACATG	1320
DB	1261	CATGTGCAGTGTGAGTTCAGGACGCGGTGGAAAGCCCTTTTGTGCTTGGACATG	1320
QY	1321	GAAGACTGTGGCTACAACTTCCACAGACATGAGTCAACCTCATGACCATAGCCTAT	1380
DB	1321	GAAGACTGTGGCTACAACTTCCACAGACATGAGTCAACCTCATGACCATAGCCTAT	1380
QY	1381	GTCTGGTGTGCTTGGCCCTTTCATGTGCTGCTTTCATGTGCTGCTGCTGCTGCTG	1440
DB	1381	GTCTGGTGTGCTTGGCCCTTTCATGTGCTGCTTTCATGTGCTGCTGCTGCTGCTG	1440
QY	1441	CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1500
DB	1441	CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1500
QY	1501	AACTGAGGAGGCGCCATGGGCAAGATAGAGATTCCTTGGACACACTCCCTGCTTCA	1560
DB	1501	AACTGAGGAGGCGCCATGGGCAAGATAGAGATTCCTTGGACACACTCCCTGCTTCA	1560
QY	1561	CTTTGGTCAACAAGTAGGAGACACAGATGGACCTGTGGCCAGAGCACCTCAGACCTCC	1620
DB	1561	CTTTGGTCAACAAGTAGGAGACACAGATGGACCTGTGGCCAGAGCACCTCAGACCTCC	1620
QY	1621	GCACCCCAAAATGCTCTGCTGCTTGTATGGAGAGGAAAGGCTGCAAGGTGGTCCAG	1680
DB	1621	GCACCCCAAAATGCTCTGCTGCTTGTATGGAGAGGAAAGGCTGCAAGGTGGTCCAG	1680
QY	1681	GGACTGTACTCTGTAGGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1740
DB	1681	GGACTGTACTCTGTAGGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1740
QY	1741	CTTGGTCACTCAAAATTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAAGCTTCA	1800
DB	1741	CTTGGTCACTCAAAATTAAGTCGGGAAATTTCTGCTGCTTGAACCTTCAAGCTTCA	1800

Qy	721	GACCACTCGCTGTACACAGCGCAGTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGCGCAGTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT	780
Qy	781	GAGGTATCATCTGTGCGGCTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840
Db	781	GAGGTATCATCTGTGCGGCTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG	840
Qy	841	TACAACATATGACAAGAGCATTTGTGGACAGTGGCACCAACCAACTTCGTTGCCCAAGAAA	900
Db	841	TACAACATATGACAAGAGCATTTGTGGACAGTGGCACCAACCAACTTCGTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGACAGCCTCTCCACGGAGAAAGTTCCTGTAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAAATCCATCAAGGACAGCCTCTCCACGGAGAAAGTTCCTGTAT	960
Qy	961	GGTTTCTGGCTAGGAGACAGCTGGTGTCTGGCAAGCAGGACCAACCCCTTTGGAAACATT	1020
Db	961	GGTTTCTGGCTAGGAGACAGCTGGTGTCTGGCAAGCAGGACCAACCCCTTTGGAAACATT	1020
Qy	1021	TTCCAGTCAATCTCACTCTACCTAATTTGGGTGAGGTTTACCAACGAGTCTTCCGCATCACC	1080
Db	1021	TTCCAGTCAATCTCACTCTACCTAATTTGGGTGAGGTTTACCAACGAGTCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGAGCAATACCTCGCGCCAGTGGAAAGATGTGGCCACAGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGAGCAATACCTCGCGCCAGTGGAAAGATGTGGCCACAGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCATCTCACAGTCATCCACGGGCAGCTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCATCTCACAGTCATCCACGGGCAGCTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACCTGTCTTTTGATCGGGCCGAAAAACGAATTTGGCTTTGCTGTACGCGCTTGC	1260
Db	1201	GGCTTCTACCTGTCTTTTGATCGGGCCGAAAAACGAATTTGGCTTTGCTGTACGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAAGGCGCTTTTGTCACTTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAAGGCGCTTTTGTCACTTTGGACATG	1320
Qy	1321	GAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1380
Db	1321	GAGACTGTGGCTACAACTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	1380
Qy	1381	GTCAATGGCTGCCATCTCGCCCTTTCATGCTGCCACTGTGCCCTCATGTGTGTCTAGTGG	1440
Db	1381	GTCAATGGCTGCCATCTCGCCCTTTCATGCTGCCACTGTGCCCTCATGTGTGTCTAGTGG	1440
Qy	1441	CGCTGCCCTCGCTGCCCTCGCCAGCAGCATGATGACTTTTCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCCTCGCTGCCCTCGCCAGCAGCATGATGACTTTTCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAAGTGAGGAGGCCCATGGCAGAGATAGAGATTCCTCGTGGACACACCTTCCTGGTTCA	1560
Db	1501	AAAGTGAGGAGGCCCATGGCAGAGATAGAGATTCCTCGTGGACACACCTTCCTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACCTCAGACCCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACCTCAGACCCCTCC	1620
Qy	1621	CCACCCACCAATGCCTCTGCCTTTGATGGAGAGAAAGGCTGGCAAGTGGGTCTCCAG	1680
Db	1621	CCACCCACCAATGCCTCTGCCTTTGATGGAGAGAAAGGCTGGCAAGTGGGTCTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAAGACATCTGCTGGCGGGAATACAT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAAGACATCTGCTGGCGGGAATACAT	1740
Qy	1741	CTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGTTGAAACTTTCAGCCTGAACT	1800
Db	1741	CTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGTTGAAACTTTCAGCCTGAACT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTTCTCCAAACCCAAAGATTTCTCTTTTCTTAGTTTCAGAA	1860

D	b		1801	TGTGTCACCATCCCTTTAAATTCCTCAACCCAAAGATTCTTCTTTCTTAGTTTCAGAA	1861
Q	y		1861	GTA	1920
D	b		1861	GTA	1920
Q	y		1921	AGACC	1980
D	b		1921	AGACC	1980
Q	y		1981	TGCTTTAGACAGCGGACTGTATAAACAAGCCCTAACATTGGTGCAAAAGATTGCCTCTTTGA	2040
D	b		1981	TGCTTTAGACAGCGGACTGTATAAACAAGCCCTAACATTGGTGCAAAAGATTGCCTCTTTGA	2040
Q	y		2041	ATTAAAAAAA	2070
D	b		2041	ATTAAAAAAA	2070
 RESULT 3 AAD13021 standard; cDNA; 2070 BP.					
X	X		AAD13021;		
X	X		23-OCT-2001 (first entry)		
D	E		Human aspartyl protease 2a (Hu-Asp2a) cDNA.		
K	W		Human; aspartyl protease 2a; Asp 2a; beta-amylold precursor protein; APP;		
K	W		beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;		
K	W		neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;		
K	W		neuroprotective; antisense therapy; gene therapy;		
K	W		chromosome 11q23.3-24.1; ss.		
X	S		Homo sapiens.		
O	S				
X	X		Key Location/Qualifiers		
F	H		CDS 1..1506		
F	T		/tag= a		
F	T		/product= "Human aspartyl protease 2a (Hu-Asp2a)"		
F	T		sig_peptide 1..63		
F	T		/tag= b		
F	T		mat_peptide 64..1503		
F	T		/tag= c		
F	T		/product= "Mature human aspartyl protease 2a (Hu-Asp2a)"		
X	N		WO200150829-A2		
X	N		19-JUL-2001.		
X	X		09-MAY-2001; 2001WO-IB00799.		
P	D		09-MAY-2001; 2001WO-IB00799.		
X	X		(BIEN/) BIENKOWSKI M J.		
P	A		(GURN/) GURNEY M E.		
P	A		(HEIN/) HEINIKSON R L.		
P	A		(PARO/) PARODI L A.		
P	A		(YANR/) YAN R.		
X	X		Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;		
P	I		WPI; 2001-483072/52.		
D	R		P-PSDB; AAE06859.		
X	X		Novel purified polypeptide comprising fragment of mammalian aspartyl		
P	T		protease 2, lacking Asp2 transmembrane domain and retaining beta		
P	T		secretase activity of Asp2 useful for identifying inhibitors of Asp2		
P	T		activity		
X	S		Claim 98; Fig 2; 185pp; English.		

Db 541 GGGCTGGCTATGCTGAGATGGCAGGCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
QY 601 CTGTAAGACAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTTGTGTGCTGGCTTC 660
Db 601 CTGTAAGACAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTTGTGTGCTGGCTTC 660
QY 661 CCCTCAACAGTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGTATC 720
Db 661 CCCTCAACAGTCTGAAGTGTGGCTCTGTGCGAGGAGCATGATCATTTGGAGTATC 720
QY 721 GACCACTCGCTGACACAGCAGTCTGTGTATACACCCATCCGGGGAGTGGTATTAT 780
Db 721 GACCACTCGCTGACACAGCAGTCTGTGTATACACCCATCCGGGGAGTGGTATTAT 780
QY 781 GAGTCTATCATTTGTGGGGTGGAGTCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
Db 781 GAGTCTATCATTTGTGGGGTGGAGTCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
QY 841 TACAATATGACAGAGCATTTGGAGTGGACAGTGGACACCAACCTTCGTTTGGCCCAAGAAA 900
Db 841 TACAATATGACAGAGCATTTGGAGTGGACAGTGGACACCAACCTTCGTTTGGCCCAAGAAA 900
QY 901 GTGTTTGAAGCTGCAGTCAATCCATCAAGSCAGCCTCTCCACGAGAGTTCCTCTGAT 960
Db 901 GTGTTTGAAGCTGCAGTCAATCCATCAAGSCAGCCTCTCCACGAGAGTTCCTCTGAT 960
QY 961 GGTTCCTGGCTAGGAGAGCAGTGGTGTGCTGCAAGCAGCACCACCTTCGTTTGGACATT 1020
Db 961 GGTTCCTGGCTAGGAGAGCAGTGGTGTGCTGCAAGCAGCACCACCTTCGTTTGGACATT 1020
QY 1021 TTCCAGTATCATCTCTACCTTAATGGGTGAGTTTACCAACAGTCTTCCTCCATCACC 1080
Db 1021 TTCCAGTATCATCTCTACCTTAATGGGTGAGTTTACCAACAGTCTTCCTCCATCACC 1080
QY 1081 ATCTTCCGAGCAATACCTTCGCGCCAGTGGAGATGTGGCCAGCTCCCAAGAGCAGTGT 1140
Db 1081 ATCTTCCGAGCAATACCTTCGCGCCAGTGGAGATGTGGCCAGCTCCCAAGAGCAGTGT 1140
QY 1141 TACAAGTTTGGCTATCATCTACCTTAATGGGTGAGTTTACCAACAGTCTTCCTCCATCACC 1200
Db 1141 TACAAGTTTGGCTATCATCTACCTTAATGGGTGAGTTTACCAACAGTCTTCCTCCATCACC 1200
QY 1201 GGTCTTACGTTGTCTTGTGATCGGGCCGAGAAACAGTGTGCTGTCAGCGCTTC 1260
Db 1201 GGTCTTACGTTGTCTTGTGATCGGGCCGAGAAACAGTGTGCTGTCAGCGCTTC 1260
QY 1261 CATGTGCACCATGATTCAGGAGCGGAGCGGTGGAGGCGCTTTTGTACCTTTGGACATG 1320
Db 1261 CATGTGCACCATGATTCAGGAGCGGAGCGGTGGAGGCGCTTTTGTACCTTTGGACATG 1320
QY 1321 GAAGACTGTGGCTTACACATTCACACAGATGAGTCAACCTTCATGACCATAGCCTAT 1380
Db 1321 GAAGACTGTGGCTTACACATTCACACAGATGAGTCAACCTTCATGACCATAGCCTAT 1380
QY 1381 GTATGCTGCCATTCGCGCCCTCTTCATGCTGCACTCTGCTCATGATGATCTCCCTGCTG 1440
Db 1381 GTATGCTGCCATTCGCGCCCTCTTCATGCTGCACTCTGCTCATGATGATCTCCCTGCTG 1440
QY 1441 CGTGTCTCGCTGCTGCGCCAGCAGCATGATGATCTTCCTGATGATGATCTCCCTGCTG 1500
Db 1441 CGTGTCTCGCTGCTGCGCCAGCAGCATGATGATCTTCCTGATGATGATCTCCCTGCTG 1500
QY 1501 AAGTGAAGGAGGCGCCATGGGAGAGATAGAGATTCCTCCCTGAGCAGCAGCTCCCTGGTTCA 1560
Db 1501 AAGTGAAGGAGGCGCCATGGGAGAGATAGAGATTCCTCCCTGAGCAGCAGCTCCCTGGTTCA 1560
QY 1561 CTTTGTGTCACAGTAGGAGACAGATGAGCAGCTGTGGCCAGAGCAGCTCCAGACCCCTCC 1620
Db 1561 CTTTGTGTCACAGTAGGAGACAGATGAGCAGCTGTGGCCAGAGCAGCTCCAGACCCCTCC 1620
QY 1621 CCACCCACCAATGCTCTGCTTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

Db 1621 CCACCCACCAATGCTCTGCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
QY 1681 GGACTGTACCTGTAGAAACAGAAAGAGAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAG 1740
Db 1681 GGACTGTACCTGTAGAAACAGAAAGAGAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAG 1740
QY 1741 CTTGGTCACTCAAAATTTAAGTGGGAAATTTCTGCTGCTTTGAAACTTCAGCCCTGAACCT 1800
Db 1741 CTTGGTCACTCAAAATTTAAGTGGGAAATTTCTGCTGCTTTGAAACTTCAGCCCTGAACCT 1800
QY 1801 TTGTCACCACTTCTTTAAATTTCTCCAAACCAAGATATTTCTTTTCTTTAGTTTCAGAA 1860
Db 1801 TTGTCACCACTTCTTTAAATTTCTCCAAACCAAGATATTTCTTTTCTTTAGTTTCAGAA 1860
QY 1861 GTACTGGCATCACAGCAGGTTACCTTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 1861 GTACTGGCATCACAGCAGGTTACCTTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1921 AGACCAAGCTTGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 AGACCAAGCTTGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1981 TGCTTTAGACACAGGAGGACTTATAAACAAGCTTAAACATTTGCTGCAAGATTTGCTCTTGA 2040
Db 1981 TGCTTTAGACACAGGAGGACTTATAAACAAGCTTAAACATTTGCTGCAAGATTTGCTCTTGA 2040
QY 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
Db 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
RESULT 5
AAS11702
ID AAS11702 standard; DNA; 2070 BP.
XX AAS11702;
XX 24-OCT-2001 (first entry)
XX DNA encoding human aspartyl protease 2a (Asp-2a).
DE Human; aspartyl protease 1; Asp-1; nontropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..1506
FT /*tag= a
FT /product= "Aspartyl protease-2a (Asp-2a)"
FT sig_peptide 1..63
FT /*tag= b
FT misc_feature 64..135
FT /*tag= c
FT /note= "Pre-propeptide"
FT misc_feature 136..171
FT /*tag= d
FT /note= "Propeptide"
FT mat_peptide 172..1503
FT /*tag= e
FT /note= "Mature Aspartyl protease-2a"
XX WO200149097-A2. ✓
XX 12-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00797.
XX 09-MAY-2001; 2001WO-IB00797.
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
PA

Db 1735 GGCACCAGCAGCGCATCCGGCTGCGCTGCGCAGCGGCGCTGGGGGCGCCCGCCCTGGG 1794
Qy 121 CTGGCGCTGCCCGGGAGACCGAGACCGAGAGCGCGGAGCGCGCGGGAGCGAGCTTT 180
Db 1795 CTGGCGCTGCCCGGGAGACCGAGACCGAGAGCGCGGAGCGCGCGGGAGCGAGCTTT 1854
Qy 181 GTGGAGATGTTGGACAACCTTGAGGGGCAAGTTCGGGGCAGGCTACTACGTGGAGATGACC 240
Db 1855 GTGGAGATGTTGNACACCTTGAGGGGCAAGTTCGGGGCAGGCTACTACGTGGAGATGACC 1914
Qy 241 GTGGGACGCCCCCGCAGAGCGCTCAACATCCTGGTGGATACAGACGACGATACCTTTGCA 300
Db 1915 GTGGGACGCCCCCGCAGAGCGCTCAACATCCTGGTGGATACAGACGACGATACCTTTGCA 1974
Qy 301 GTGGGTGCTGCCCGCCCGCCCTTCTCGATCGCTACTACAGAGCGAGCTGCCAGACA 360
Db 1975 GTGGGTGCTGCCCGCCCGCCCTTCTCGATCGCTACTACAGAGCGAGCTGCCAGACA 2034
Qy 361 TACCGGACCTCCGGAAGGTTGTATGTGCGCTTACACCGAGGCAAGTGGGAAGGGAG 420
Db 2035 TACCGGACCTCCGGAAGGTTGTATGTGCGCTTACACCGAGGCAAGTGGGAAGGGAG 2094
Qy 421 CTGGGACGACCTGGTAAAGATCCCGCATGGCCCGCAAGCTCACTGTGCGTGCACATTT 480
Db 2095 CTGGGACGACCTGGTAAAGATCCCGCATGGCCCGCAAGCTCACTGTGCGTGCACATTT 2154
Qy 481 GCTGCCATCACTGAATCAGACAAGTCTTCAACAACGCTCCAACTGGGAAGGATCCTG 540
Db 2155 GCTGCCATCACTGAATCAGACAAGTCTTCAACAACGCTCCAACTGGGAAGGATCCTG 2214
Qy 541 GGGCTGCGCTATGTGAGATGGCAGGCGCTGACGACTCCCTGGAGCGCTTCTTTGACTCT 600
Db 2215 GGGCTGCGCTATGTGAGATGGCAGGCGCTGACGACTCCCTGGAGCGCTTCTTTGACTCT 2274
Qy 601 CTGTAAGCAGACCGACGCTCCCAACCTCTTCTCCCTGCACTTCTGCTGCGTGCCTTC 660
Db 2275 CTGTAAGCAGACCGACGCTCCCAACCTCTTCTCCCTGCACTTCTGCTGCGTGCCTTC 2334
Qy 661 CCCCTCAACAGTCTGAAGTCTGGCGCTCTGCGAGGAGGAGCATGATCATTTGGAGTATC 720
Db 2335 CCCCTCAACAGTCTGAAGTCTGGCGCTCTGCGAGGAGGAGCATGATCATTTGGAGTATC 2394
Qy 721 GACCATCGCTGTACAGGCGAGTCTCTGGTATACACCCATCCCGGGGAGTGGTATAT 780
Db 2395 GACCATCGCTGTACAGGCGAGTCTCTGGTATACACCCATCCCGGGGAGTGGTATAT 2454
Qy 781 GAGTCTCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 840
Db 2455 GAGTCTCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAATGGACTGCAAGGAG 2514
Qy 841 TACAATATGACAAGACGATTTGGACAGTGGCAGTGGCACCAACCTTCGTTTGGCCCAAGAA 900
Db 2515 TACAATATGACAAGACGATTTGGACAGTGGCAGTGGCACCAACCTTCGTTTGGCCCAAGAA 2574
Qy 901 GTGTTTGAAGTGCAGTCAATCATCAAGCAGCGCTCCCTCCAGGAGAGTTCCTCGAT 960
Db 2575 GTGTTTGAAGTGCAGTCAATCATCAAGCAGCGCTCCCTCCAGGAGAGTTCCTCGAT 2634
Qy 961 GTTTCCTGCTGAGGAGCAGCTGGTGTGCTGCAAGCAGGACCAACCTTCGTTTGGCAACAT 1020
Db 2635 GTTTCCTGCTGAGGAGCAGCTGGTGTGCTGCAAGCAGGACCAACCTTCGTTTGGCAACAT 2694
Qy 1021 TTCCAGTATCTCACTCTACCTAATGGTGGAGTTTACCAACAGTCTTCCCGCATCACC 1080
Db 2695 TTCCAGTATCTCACTCTACCTAATGGTGGAGTTTACCAACAGTCTTCCCGCATCACC 2754
Qy 1081 ATCCTTCGCGAGCAATACCTCGCGCAGTGAAGATGTGGCCAGTCCCAAGAGCTGT 1140
Db 2755 ATCCTTCGCGAGCAATACCTCGCGCAGTGAAGATGTGGCCAGTCCCAAGAGCTGT 2814
Qy 1141 TACAAGTTTGGCATCTCACAGTCTATCCAGCGGCACTGTTATGGAGTGTATCATGGAG 1200
Db 2815 TACAAGTTTGGCATCTCACAGTCTATCCAGCGGCACTGTTATGGAGTGTATCATGGAG 2874

Qy 1201 GGCTTCTACGTTGCTTTTGTATCGGCGCCGAAACGAATTTGGCTTTGCTGTACGCGTTGC 1260
Db 2875 GCCTTCTACGTTGCTTTTGTATCGGCGCCGAAACGAATTTGGCTTTGCTGTACGCGTTGC 2934
Qy 1261 CATGTCCAGATGAGTTTCAGGACGCGCGGTGGAAGGCCCTTTTGTACCTTTGGACATG 1320
Db 2935 CATGTCCAGATGAGTTTCAGGACGCGCGGTGGAAGGCCCTTTTGTACCTTTGGACATG 2994
Qy 1321 GAAGACTGGGCTACACATTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT 1380
Db 2995 GAAGACTGGGCTACACATTTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT 3054
Qy 1381 GTCATGGCTGCCATCTGCGCCCTTTCATGCTGCCACTCTGCTCATGTTGTTGTCTAGTGG 1440
Db 3055 GTCATGGCTGCCATCTGCGCCCTTTCATGCTGCCACTCTGCTCATGTTGTTGTCTAGTGG 3114
Qy 1441 CGTGTCTCGCTGCGCTGCCAGCAGATGATGACTTTTCTGCTGATGACATCTCCCTGCTG 1500
Db 3115 CGTGTCTCGCTGCGCTGCCAGCAGATGATGACTTTTCTGCTGATGACATCTCCCTGCTG 3174
Qy 1501 AAGTGAGGAGGCCCATGGGCGAGAGATAGAGATTTCCCTGCGACACACCTCCGTTGTTCA 1560
Db 3175 AAGTGAGGAGGCCCATGGGCGAGAGATAGAGATTTCCCTGCGACACACCTCCGTTGTTCA 3234
Qy 1561 CTTTGTGTACAAAGTAGGAGACACAGATGGCACCTGTGGCGAGAGACCTCAGACCCCTCC 1620
Db 3235 CTTTGTGTACAAAGTAGGAGACACAGATGGCACCTGTGGCGAGAGACCTCAGACCCCTCC 3294
Qy 1621 CCACCCACCAATTCCTCTGCTGCTGATGGAGAGAGAAAGCTGGCAGAGTGGGTTCCAG 1680
Db 3295 CCACCCACCAATTCCTCTGCTGCTGATGGAGAGAGAAAGCTGGCAGAGTGGGTTCCAG 3354
Qy 1681 GGACTGTACCTGTAGGAAACAGAGAGAGAAAGAACACCTCTGCTGGCGGAATACT 1740
Db 3355 GGACTGTACCTGTAGGAAACAGAGAGAGAAAGAACACCTCTGCTGGCGGAATACT 3414
Qy 1741 CTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTTGAACTTCAGCCCTGAACT 1800
Db 3415 CTTGGTCACTCAAAATTTAAGTCGGGAAATTTCTGCTGCTTTGAACTTCAGCCCTGAACT 3474
Qy 1801 TTGTCACCACTTCTTTAAATTTCCAAACCAAGATTTCTCTTTTCTTAGTTTCAGAA 1860
Db 3475 TTGTCACCACTTCTTTAAATTTCCAAACCAAGATTTCTCTTTTCTTAGTTTCAGAA 3534
Qy 1861 GTACTGTCATCACACGAGGTTACCTTGGCGTGTGTCCTGTTGTAACCTTCAGCCCTGAGAG 1920
Db 3535 GTACTGTCATCACACGAGGTTACCTTGGCGTGTGTCCTGTTGTAACCTTCAGCCCTGAGAG 3594
Qy 1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGGATGACAGTTTGTCTATT 1980
Db 3595 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGGATGACAGTTTGTCTATT 3654
Qy 1981 TGCTTTAGACAGAGGAGTGTATAAACAAGCTTAACATTTGGTCAAAAGATTGCTCTTTGA 2040
Db 3655 TGCTTTAGACAGAGGAGTGTATAAACAAGCTTAACATTTGGTCAAAAGATTGCTCTTTGA 3714
Qy 2041 ATTAATAAAAAAAAAAAAAA 2059
Db 3715 ATTAATAAAAAAAAAACTAGA 3733

RESULT 10

AAA59551

ID AAA59551 standard; DNA; 2348 BP.

XX AAA59551;

AC AC

XX 14-NOV-2000 (first entry)

DT DNA encoding a human beta-secretase enzyme.

DE Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
XX
KW

Qy	1441	CGTGTGCTCGCTGCTGGCCAGCAGCATGATGACTTTGGCTGATGACATCTCCCTGCTG	1500
Db	1746	CGTGTGCTCGCTGCTGGCCAGCAGCATGATGACTTTGGCTGATGACATCTCCCTGCTG	1805
Qy	1501	AAGTGAGGAGGCCATGGCAGAAAGATAGAGATTCCTCCCTGGACACACCTCCGCTGTTCA	1560
Db	1806	AAGTGAGGAGGCCATGGCAGAAAGATAGAGATTCCTCCCTGGACACACCTCCGCTGTTCA	1865
Qy	1561	CTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACACCTCAGGACCCCTCC	1620
Db	1866	CTTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGACACCTCAGGACCCCTCC	1925
Qy	1621	CCACCCACCAATGCCTCTGCCCTTGATGGAGAAAGGCGTGGCAAGGTGGGTTCACG	1680
Db	1926	CCACCCACCAATGCCTCTGCCCTTGATGGAGAAAGGCGTGGCAAGGTGGGTTCACG	1985
Qy	1681	GGACTGTACCTGTAGGAACAGAAAGAGAAAGAAAGACACCTCTGCTGCGCGGAATACT	1740
Db	1986	GGACTGTACCTGTAGGAACAGAAAGAGAAAGAAAGACACCTCTGCTGCGCGGAATACT	2045
Qy	1741	CTTTGGTCACCTCAAAATTTAAGTCGGGAAATTTGCTGCTTTGAAACTTCAGCCCTGAACCT	1800
Db	2046	CTTTGGTCACCTCAAAATTTAAGTCGGGAAATTTGCTGCTTTGAAACTTCAGCCCTGAACCT	2105
Qy	1801	TTGTCCACCAATTCCTTTAAATTTCTCAACCAAGATATCTCTTTCTTTAGTTTCAGAA	1860
Db	2106	TTGTCCACCAATTCCTTTAAATTTCTCAACCAAGATATCTCTTTCTTTAGTTTCAGAA	2165
Qy	1861	GTACTGGCATCACACGAGGTTACCTTTGGCGTGTGTCCTCTGGTACCCCTGGCAGAGAAG	1920
Db	2166	GTACTGGCATCACACGAGGTTACCTTTGGCGTGTGTCCTCTGGTACCCCTGGCAGAGAAG	2225
Qy	1921	AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTGCTATT	1980
Db	2226	AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGATGCACAGTTTGCTATT	2285
Qy	1981	TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTTGGTCAAAAGATTGCTCTTTGA	2040
Db	2286	TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTTGGTCAAAAGATTGCTCTTTGA	2345
Qy	2041	ATT 2043	
Db	2346	ATT 2348	

RESULT 11

AAV41696

ID AAV41696 standard; cDNA: 2541 BP.

RESULT 11
AAV41696
ID AAV41696 standard; cDNA; 2541 BP.

AAV41696;

DT · 26-OCT-1998 (first entry)

XX Nucleotide sequence of human ASP2 (aspartic protease 2).

XX Human; ASP2; aspartic protease 2; agonist; antagonist; immunospecific;
KW antibody; inhibition; Alzheimer's disease; cancer; proteinase;
KW prohormone processing; ss.

XX Homo sapiens. OS

XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..1506
FT /*tag= a
FT /product= "human ASP2"

PN EP855444-A2.

XX
PD
29-JUL-1998

XX
27-TAN-1998. : 98EP-0300573
PF

XX
PR 28-JAN-1997; 97GB-0001684.

CC	memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2	
CC	isolation, purification and characterisation.	
xx		
sq	Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;	
	Query Match 97.1%; Score 2010; DB 22; Length 3252;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Qy	40 GCGGGAGTGTGCTGCCACCGGACCCAGCAGGCAATCCGGTGGCCCTGGCGAGGGC 99	
Db	1 GCGGGAGTGTGCTGCCACCGGACCCAGCAGGCAATCCGGTGGCCCTGGCGAGGGC 60	
Qy	100 CTGGGGGGCCCCCTGGGGCTGGCGTGGCCGGGAGACCGGACGAGAGCCCGAGGAG 159	
Db	61 CTGGGGGGGGCCCCCTGGGGCTGGCGTGGCCGGGAGACCGGACGAGAGCCCGAGGAG 120	
Qy	160 CCCGGCGGAGGGCAGCTTTGTGGAGATGGTGACAACTTGAGGGGCAAGTCGGGGCAG 219	
Db	121 CCCGGCGGAGGGCAGCTTTGTGGAGATGGTGACAACTTGAGGGGCAAGTCGGGGCAG 180	
Qy	220 GGCTACTACGTGGAGATGACCGTGGGAGAGCCCCCGGAGAGCGCTCAACATCCTGGTGGAT 279	
Db	181 GGCTACTACGTGGAGATGACCGTGGGAGAGCCCCCGGAGAGCGCTCAACATCCTGGTGGAT 240	
Qy	280 ACAGGCAGCAGTAACCTTTGACAGTGGTGTGCTGCCCGCCACCCCTTCCTGCATCGCTACTAC 339	
Db	241 ACAGGCAGCAGTAACCTTTGACAGTGGTGTGCTGCCCGCCACCCCTTCCTGCATCGCTACTAC 300	
Qy	340 CAGAGGCAGCTGTCCAGACATACCGGAGACCTCCGGAGAGGTGTGTATGTGCCCTACACC 399	
Db	301 CAGAGGCAGCTGTCCAGACATACCGGAGACCTCCGGAGAGGTGTGTATGTGCCCTACACC 360	
Qy	400 CAGGCAGTGGAGGGAGCTGGGACCGACCTGTGAGCATCCCGCCATGGCCCGCCAAAC 459	
Db	361 CAGGCAGTGGAGGGAGCTGGGACCGACCTGTGAGCATCCCGCCATGGCCCGCCAAAC 420	
Qy	460 GTCACTGTGCGTGCCCAACTGTGCTGCTCACTACTGAATCAGACAAAGTTCTTCAACAGGC 519	
Db	421 GTCACTGTGCGTGCCCAACTGTGCTGCTCACTACTGAATCAGACAAAGTTCTTCAACAGGC 480	
Qy	520 TCCAACTGGGAGGAGTCTGGGGCTGGCCCTATGCTGAGATGGCAGGCTGAGACTCC 579	
Db	481 TCCAACTGGGAGGAGTCTGGGGCTGGCCCTATGCTGAGATGGCAGGCTGAGACTCC 540	
Qy	580 CTGAGGCTTTCTTTGACTCTCTGTAAAGCAGACCCACGTTGCCAACCTCTCTCCCTG 639	
Db	541 CTGAGGCTTTCTTTGACTCTCTGTAAAGCAGACCCACGTTGCCAACCTCTCTCCCTG 600	
Qy	640 CACCTTTGTGTGTGCTTCCCGCTCAACCACTGTGAAGTGTGGCTCTGTGCGAGGG 699	
Db	601 CAGCTTTGTGTGTGCTTCCCGCTCAACCACTGTGAAGTGTGGCTCTGTGCGAGGG 660	
Qy	700 AGCATGATCATGGAGGTATCGACCACTCGCTGTACAGAGCAGTCTGTGTATACACC 759	
Db	661 AGCATGATCATGGAGGTATCGACCACTCGCTGTACAGAGCAGTCTGTGTATACACC 720	
Qy	760 ATCCGGCGGGAGTGTGATTTATGAGGTATCATTTGTGGGGTGGAGATCAATGGACAGAT 819	
Db	721 ATCCGGCGGGAGTGTGATTTATGAGGTATCATTTGTGGGGTGGAGATCAATGGACAGAT 780	
Qy	820 CTGAAATGGATGCAAGAGTACAACTATGACAGAGCATTTGGAGCAGTGGCACACC 879	
Db	781 CTGAAATGGATGCAAGAGTACAACTATGACAGAGCATTTGGAGCAGTGGCACACC 840	
Qy	880 RACCTTCCTTTGCCCAAGAGTGTTCGAAGCTGAGTCAATCCATCAAGSCAGCCTCC 939	
Db	841 RACCTTCCTTTGCCCAAGAGTGTTCGAAGCTGAGTCAATCCATCAAGSCAGCCTCC 900	
Qy	940 TCCACGGAGAGTTCCTCGATGGTTCTCTGGCTAGGAGACGAGCTGGTGTGTCGCAAGCA 999	
Db	901 TCCACGGAGAGTTCCTCGATGGTTCTCTGGCTAGGAGACGAGCTGGTGTGTCGCAAGCA 960	
Qy	1000 GGCACCACCCCTTGGGAACATTTTCCAGTCATCTACTCTACTTAATGGGTAGGTTACC 1059	
Db	961 GGCACCACCCCTTGGGAACATTTTCCAGTCATCTACTCTACTTAATGGGTAGGTTACC 1020	
Qy	1060 AACCACTCCCTTCCGCATCACCATCTTCCGACGAATACCTGCGGCAGTGGAGATGTG 1119	
Db	1021 AACCACTCCCTTCCGCATCACCATCTTCCGACGAATACCTGCGGCAGTGGAGATGTG 1080	
Qy	1120 GCCACGTCCCAAGACAGCTGTTACAAGTTTGGCCATCTCACAGTCATCCAGGCACTGTT 1179	
Db	1081 GCCACGTCCCAAGACAGCTGTTACAAGTTTGGCCATCTCACAGTCATCCAGGCACTGTT 1140	
Qy	1180 ATGGGAGCTGTTATCATGAGAGGCTTCTACGTTTGTCTTTTATCGGGCCCCGAAACGAAT 1239	
Db	1141 ATGGGAGCTGTTATCATGAGAGGCTTCTACGTTTGTCTTTTATCGGGCCCCGAAACGAAT 1200	
Qy	1240 GGCTTTGTCTGACGGCTTGGCAATGTGCAGATGAGTTCAAGGAGCGGCGGTGGAGGC 1299	
Db	1201 GGCTTTGTCTGACGGCTTGGCAATGTGCAGATGAGTTCAAGGAGCGGCGGTGGAGGC 1260	
Qy	1300 CCTTTTGTCACTTGGACATGGAAGACTGTGGCTACAACATTCACACAGACAGATGAGTCA 1359	
Db	1261 CCTTTTGTCACTTGGACATGGAAGACTGTGGCTACAACATTCACACAGACAGATGAGTCA 1320	
Qy	1360 ACCCTCATGACATGAGCTATGTATGCTGGCTGGCCATCTGCGCCCTCTTTCATGCTGCCACTC 1419	
Db	1321 ACCCTCATGACATGAGCTATGTATGCTGGCTGGCCATCTGCGCCCTCTTTCATGCTGCCACTC 1380	
Qy	1420 TGCTCATGTGTGTGAGTGGCGCTGCTCCGCTGCTGCGCCAGCAGCATGATGACTTT 1479	
Db	1381 TGCTCATGTGTGTGAGTGGCGCTGCTCCGCTGCTGCGCCAGCAGCATGATGACTTT 1440	
Qy	1480 GCTGATGACATCTCCCTGCTGAAGTGAAGGAGGCCATGGGAGAGATGAGATTCCTCT 1539	
Db	1441 GCTGATGACATCTCCCTGCTGAAGTGAAGGAGGCCATGGGAGAGATGAGATTCCTCT 1500	
Qy	1540 GGCACACCTCCGTGGTTTCACTTTGCTACAGTAGGAGACAGATGGCAGCTGTGGC 1599	
Db	1501 GGCACACCTCCGTGGTTTCACTTTGCTACAGTAGGAGACAGATGGCAGCTGTGGC 1560	
Qy	1600 CAGAGCAGCTCAGGAGCCCTCCACCCACCAATGCTCTGCTTGTATGAGAGAGGAAA 1659	
Db	1561 CAGAGCAGCTCAGGAGCCCTCCACCCACCAATGCTCTGCTTGTATGAGAGAGGAAA 1620	
Qy	1660 GGCTGGCAAGTGGGTTTCCAGGGAGTACTCTGTAGGAAAACAGAAAAGAGAAAGAG 1719	
Db	1621 GGCTGGCAAGTGGGTTTCCAGGGAGTACTCTGTAGGAAAACAGAAAAGAGAAAGAG 1680	
Qy	1720 CACTCTGCTGGCGGGAATACTCTTGGTCACTCAAAATTTAAGTCGGGAAATTCCTGCTGCT 1779	
Db	1681 CACTCTGCTGGCGGGAATACTCTTGGTCACTCAAAATTTAAGTCGGGAAATTCCTGCTGCT 1740	
Qy	1780 TGAACCTTCAGCCCTGAACCTTTTGTCCACCATTCCTTTAAATTCCTCAACCCCAAGTATT 1839	
Db	1741 TGAACCTTCAGCCCTGAACCTTTTGTCCACCATTCCTTTAAATTCCTCAACCCCAAGTATT 1800	
Qy	1840 CTTCCTTTCTTAGTTCAGAAAGTACTGGCATCACACAGGTTACCTTGGCGTGTGCC 1899	
Db	1801 CTTCCTTTCTTAGTTCAGAAAGTACTGGCATCACACAGGTTACCTTGGCGTGTGCC 1860	
Qy	1900 TGTGTTACCTTGGCAGAGAGAGACCAAGCTTGTTCCTGCTGCGCCAAAGTCAGTAGGA 1959	
Db	1861 TGTGTTACCTTGGCAGAGAGAGACCAAGCTTGTTCCTGCTGCGCCAAAGTCAGTAGGA 1920	
Qy	1960 GAGGATGCACAGTTTGTCTTTTGTAGACAGAGGAGCTGTATAAACAAGCCCTTAACATT 2019	
Db	1921 GAGGATGCACAGTTTGTCTTTTGTAGACAGAGGAGCTGTATAAACAAGCCCTTAACATT 1980	
Qy	2020 GGTGCAAGATGCTCTTGAATTTAAAAAATAAAAAA 2057	
Db	1981 GGTGCAAGATGCTCTTGAATTTAAAAAATAAAAAA 2018	

RESULT 13	
AAE28101	
ID AAF28101 standard; DNA; 3252 BP.	
XX AC	
XX AC	
AAF28101;	
XX AC	
DT 02-APR-2001 (first entry)	
XX AC	
XX DE	
XX DE	
KW Memapsin 2 DNA.	
XX AC	
OS Memapsin 2; catalyst; Alzheimer's; ds.	
XX OS	
XX Homo sapiens.	
PN WO200100663-A2.	
PD 04 - JAN - 2001.	
XX PF	
PF 27 - JUN - 2000; 2000WO-US17661.	
XX PR	
PR 28 - JUN - 1999; 99US-0141363.	
PR 30 - NOV - 1999; 99US-0168060.	
PR 25 - JAN - 2000; 2000US-0177836.	
PR 27 - JAN - 2000; 2000US-0178368.	
PR 08 - JUN - 2000; 2000US-0210292.	
XX PR	
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.	
XX PA	
PI Tang JUN, Lin X, Koelsch G;	
XX PI	
XX DR WPI; 2001-102885/11.	
XX DR	
DR Purified recombinant catalytically active memapsin 2, used to screen inhibitors of it, which are used to treat and prevent Alzheimer's disease -	
PT PT	
PT PT	
PS Example 1; Page 71-72; 86pp; English.	
XX PS	
CC The present invention relates to a purified recombinant catalytically active memapsin 2. The invention may be used for isolating inhibitors which are used to treat or prevent Alzheimer's disease. The invention may also be used to screen for individuals more genetically prone to develop Alzheimer's disease.	
XX CC	
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;	
Query Match 97.1%; Score 2010; DB 22; Length 3252;	
Best Local Similarity 99.8%; Pred. No. 0;	
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
40 GCGGAGTGTCTGCCACGGCACCAGCACGGCATCGGCTGCCCTCGGCAGGGC 99	
1 GCGGAGTGTCTGCCACGGCACCAGCACGGCATCGGCTGCCCTCGGCAGGGC 60	
100 CTGGGGGCGCCCCCTCGGGCTCGGGTGCCCGGGAGACCGACGAAGACCCCGAGGAG 159	
61 CTGGGGGCGCCCCCTCGGGCTCGGGTGCCCGGGAGACCGACGAAGACCCCGAGGAG 120	
160 CCCGCGCGAGGGGAGCTTTGTGGAGATGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219	
121 CCCGCGCGAGGGGAGCTTTGTGGAGATGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180	
220 GGCTACTACGTGGAGATCACCTGGGAGCCCCCGGAGAGGCTCAACATCCTCGTGGAT 279	
181 GGCTACTACGTGGAGATGACCTGGGAGCCCCCGGAGAGGCTCAACATCCTCGTGGAT 240	
280 ACAGGCAGCAGTAACCTTTGTGAGTGGGTGCTGCCCGCCCACCCCTTCCTGCACTGCTACTAC 339	
241 ACAGGCAGCAGTAACCTTTGTGAGTGGGTGCTGCCCGCCCACCCCTTCCTGCACTGCTACTAC 300	
340 CAGAGGCAGCTGTCCAGCACATACCGGAGACCTCCGGGAAGGGTGTGTATGTGCCCTACACC 399	

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QY 1480 GCTGATGACATCTCCCTGCTGAAGTGAAGGAGGAGGCCCATGGCAGAGATAGAGATTCCCT 1539
Db 1441 GCTGATGACATCTCCCTGCTGAAGTGAAGGAGGAGGCCCATGGCAGAGATAGAGATTCCCT 1500
QY 1540 GGACACACCTCCGTTGGTTCAGTGTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1599
Db 1501 GGACACACCTCCGTTGGTTCAGTGTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
QY 1600 CAGACACCTCAGGACCTCCGCCACCCACCAATGCTCTGCTGTGATGGAGAGAA 1659
Db 1561 CAGACACCTCAGGACCTCCGCCACCCACCAATGCTCTGCTGTGATGGAGAGAA 1620
QY 1660 GCTGCGAAGTGGTTCAGGAGTGTACCTGTAGGAAACAGAAAGAGAAAGAG 1719
Db 1621 GCTGCGAAGTGGTTCAGGAGTGTACCTGTAGGAAACAGAAAGAGAGAGAG 1680
QY 1720 CACTCTGCTGGCGGAATCTCTGGTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1779
Db 1681 CACTCTGCTGGCGGAATCTCTGGTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1740
QY 1780 TGAACCTCAGCCCTGACCTTTGTCACCATTCCTTTAAATTCCTCAACCAAAAGTATT 1839
Db 1741 TGAACCTCAGCCCTGACCTTTGTCACCATTCCTTTAAATTCCTCAACCAAAAGTATT 1800
QY 1840 CTTCTTTTCTAGTTTCAAGTACTTGGCATCACAGCAGGTACTTGGCGTGTGCC 1899
Db 1801 CTTCTTTTCTAGTTTCAAGTACTTGGCATCACAGCAGGTACTTGGCGTGTGCC 1860
QY 1900 TGTGTACCTCGCAGAGAGAGACCAAGCTTGTTCCTGCTGCGCAAAAGTCAGTAGA 1959
Db 1861 TGTGTACCTCGCAGAGAGAGACCAAGCTTGTTCCTGCTGCGCAAAAGTCAGTAGA 1920
QY 1960 GAGGATGACAGTTTCTGCTATTTGCTTTAGAGACAGGAGTGTATAAAGCAAGCTTAACATT 2019
Db 1921 GAGGATGACAGTTTCTGCTATTTGCTTTAGAGACAGGAGTGTATAAAGCAAGCTTAACATT 1980
QY 2020 GTGCAAGATTGCTCTTTGAATTAATAAAAAAAAAAAAA 2057
Db 1981 GTGCAAGATTGCTCTTTGAATTAATAAAAAAAAAAAAACTAGA 2018

RESULT 14
ABK88641
ID ABK88641 standard; cDNA; 3252 BP.
XX AC ABK88641;
XX 07-OCT-2002 (first entry)
cDNA encoding human memapsin 2.
XX Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nontropic; expressed sequence tag; EST; gene; ss.
XX Homo sapiens.
XX key 1-1467
XX CDS /tag- a
FT /partial
FT /product= "Memapsin 2"
FT /note= "This sequence lacks a start codon"
XX US2002049303-A1.
XX 25-APR-2002.
XX 28-FEB-2001; 2001US-0796264.
XX 28-JUN-1999; 99US-141363P.
XX 30-NOV-1999; 99US-168060P.

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PR 25-JAN-2000; 2000US-177836P.
PR 27-JAN-2000; 2000US-178368P.
PR 27-JUN-2000; 2000US-0604608.
XX (TANG/) TANG J N.
PA (LINX/) LIN X.
PA (KOEL/) KOELSCH G.
PA (HONG/) HONG L.
XX Tang JUN, Lin X, Koelsch G, Hong L;
XX WPI; 2002-507280/54.
DR P-PSDB; AAU99488.
XX New recombinant catalytically active memapsin 2, useful to screen for
PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease
XX Example 1; Page 20-21; 44pp; English.
XX The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence encodes
CC human memapsin 2.
XX Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;
SQ Query Match 97.1%; Score 2010; DB 24; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 40 GCGGAGTGTCTGCTGCCCCAGGACCCAGCAGCGCATCCGCTGCCCTCGGAGCGGC 99
Db 1 GCGGAGTGTCTGCTGCCCCAGGACCCAGCAGCGCATCCGCTGCCCTCGGAGCGGC 60
QY 100 CTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 159
Db 61 CTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
QY 150 CCGCGCGGAGGGGAGCTTTTGTGAGATGTTGTGACAACTCTGAGGGGCAAGTCGGGGCAG 219
Db 121 CCGCGCGGAGGGGAGCTTTTGTGAGATGTTGTGACAACTCTGAGGGGCAAGTCGGGGCAG 180
QY 220 GGCTACTACGTGGAGATCACCGTGGGAGCCCGCGCAGAGCTCAACATCTGTGTGAT 279
Db 181 GGCTACTACGTGGAGATCACCGTGGGAGCCCGCGCAGAGCTCAACATCTGTGTGAT 240
QY 280 ACAGGACAGTACTTTTGCATGGTGGTGTGCTGCCCGCCCGCCCTTCTGCTGCTACTAC 339
Db 241 ACAGGACAGTACTTTTGCATGGTGGTGTGCTGCCCGCCCGCCCTTCTGCTGCTACTAC 300
QY 340 CAGAGGACGTGTCCAGACATACCGGAGCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
Db 301 CAGAGGACGTGTCCAGACATACCGGAGCTCCGGAAGGGTGTGTATGTGCCCTACACC 360
QY 400 CAGGCAAGTGGGAAGGGAGCTGGGACCGGACCTGGTAAGCATCCCGCCCGCCCAAC 459
Db 361 CAGGCAAGTGGGAAGGGAGCTGGGACCGGACCTGGTAAGCATCCCGCCCGCCCAAC 420
QY 460 GTCACTGTGCGTCCCAACATTGCTGCCATCTACTGAATCAGACAAAGTCTTTCATCAACGGC 519
Db 421 GTCACTGTGCGTCCCAACATTGCTGCCATCTACTGAATCAGACAAAGTCTTTCATCAACGGC 480
QY 520 TCCAACTGGGAAGGATCTCTGGGGTGGCTGATGTGATGTCAGATGCGCAGGCTGACACTCC 579
Db 481 TCCAACTGGGAAGGATCTCTGGGGTGGCTGATGTGATGTCAGATGCGCAGGCTGACACTCC 540
QY 580 CTGGAGGCTCTTTCTTGACTCTCTGCTTAAAGCAGAGACCCAGTTCCTCCCAACCTCTTCTCCCTG 639

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Result No.	Score	Query		ID	Description
		Match	Length		
1	2070	100.0	2070	9	US-09-869-414-3
2	2070	100.0	2070	9	US-09-548-366-3
3	2070	100.0	2070	10	US-09-794-927-3
4	2070	100.0	2070	10	US-09-795-847-3
5	2070	100.0	2070	10	US-09-794-743-3
6	2070	100.0	2070	10	US-09-794-748-3
7	2070	100.0	2070	10	US-09-794-925-3
8	2070	100.0	2070	10	US-09-681-442-3
9	2032	98.2	2541	9	US-09-969-671A-1
10	2032	98.2	2541	9	US-10-308-365-1
11	2010	97.1	3252	9	US-09-795-903A-1
12	2010	97.1	3252	9	US-10-032-818-1
13	2010	97.1	3252	10	US-09-796-264-1
14	2010	97.1	3252	10	US-09-845-226-1
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RESULT 2
 US-09-548-366-3
 ; Sequence 3, Application US/09548366
 ; Publication NO. US20030104365A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bienkowski, Michael J.
 ; APPLICANT: Heinrichson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; FILE OF INVENTION: 28341/6280A
 ; CURRENT APPLICATION NUMBER: US/09/548,366

[illegible]

RESULT 3

US-09-794-927-3
RESOLV. 3
: Sequence 3, Application US-09-794927
: Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrikson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

	Query Match	100.0%;	Score 2070;	DB 10;	Length 2070;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2070;	Conservative	0;	Mismatches	0; Indels
					0; Gaps
Qy	1	ATGCCCCAAGCCCTGCCCCCTGGCTCCTGCTGTGGATGGCGCGGAGTGCCTGCCCTGCCAC	60		
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Db	61	GGCACCAGACAGCGCATCCGGCTGCCCCCTTGGCAGCGGCTTGGGGGCGCCCCCTGGGG	120		
Qy	121	CTCGGGCTGCCCGGAGACCGACGAAGAGCCCCGAGAGCCCGGCCCGAGGGGACAGCTTT	180		
Db	121	CTCGGGCTGCCCGGAGACCGACGAAGAGCCCCGAGAGCCCGGCCCGAGGGGACAGCTTT	180		
Qy	181	GTGGAGATGTGGACACCTTGAGGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC	240		
Db	181	GTGGAGATGTGGACACCTTGAGGGGCAAGTCGGGGCAGGCTACTACGTGGAGATGACC	240		
Qy	241	GTGGGCGAGCCCCCGCAGAGCGCTCAACATCCTGTGGTATACAGCAGCAGCTAACTTTGCA	300		
Db	241	GTGGGCGAGCCCCCGCAGAGCGCTCAACATCCTGTGGTATACAGCAGCAGCTAACTTTGCA	300		

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RESULT 4
US-09-795-847-3
; Sequence 3, Application US/09795847
; Patent No. US20010018208A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Helmrison, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-847-3

Query Match 100.0%; Score 2070; DB 10; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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481	Db	GCTGCCATCACTGAATCAGACAAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTGT	540
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541	Db	GGGCTGCCCTATGCTGAGATTGCCAGGCTTGAGGACCTCCCTGGAGCGCTTCTTTTGACTCT	600
601	Qy	CTGСТААAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTTGTGTGGTGGCTTC	660
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1021	Db	TTCCGAGCTCATCTCACTTACCTAATGGGTGAGGTTACCAACAGTCCCTTCCGAGATCACC	1080
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1081	Db	ATCCTTCCGAGCAATACCTCGGCGCAGTGGAGATGTGCCAGTGGCCAGTCCCAAGACGACTGT	1140
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1201	Db	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAAACGAATTGGCTTGTGTGTCAGCGCTTC	1260
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RESULT 6
US-09-794-748-3
Sequence 3, Application US~~09~~794748
Patent No. US20020037315A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280JL
CURRENT APPLICATION NUMBER: US/09/794,748
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2070
TYPE: DNA

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301 GTGGGTGCTGCCCCCGGAGAGCTCAACATCTCTGTGTATACAGGAGGAGTACTTTGCA 360
361 TACCGGAGCTCCGGAGAGGTGTATGTGCCCCCTACACCCAGGCGAAGTGGGAGGGAG 420
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RESULT 11

US-09-795-903A-1
; Sequence 1, Application us/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/504,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836


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; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-795-903A-1

Query Match          97.1%; Score 2010; DB 9; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 12
US-10-Q32-818-1
; Sequence 1, Application US/10032818
; Publication No. US20030092629A1 ✓
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Koelsch, Gerald
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 2932.1006-007
; CURRENT APPLICATION NUMBER: US/10/032,818
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-Q32-818-1

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Db	661	AGCATGATCATNTGGAGGTATPGACCACCTGCTACACAGGCAGTCTCTGGTATACACCC	720
QY	760	ATCCGGGGGAGTGGTATATGAGGTATCATTTGTGCGGGTGGAGATCAATGACAGGAT	819
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QY	880	AACCTTCGTTTCCCCAAGAAAGTGTTTGAAGTGCAGTCAAAATCCATCAAGGCAGCTCC	939
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QY	940	TCCACGGAGAAGTTCCCTGATGTTTCTGCTAGGAGAGCAGCTGGTGTCTGGCAAGCA	999
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Db	586	CCCTCAACAGCTCTGAAGTGTGGCTCTGTGGAGGAGCATGATCATTTGGAGTATC	645
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QY	1561	CTTTGGTCAAGTAGGAGACACAGATGGCACTGTGGCCAGACACCTCAGACACCTCC	1620
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Job time : 507 secs

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